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OM protein - protein search, using sw model

Run on: November 1, 2004, 17:52:26 ; Search time 90 Seconds  
(without alignments)  
139.506 Million cell updates/sec

Title: US-10-802-574-3  
Perfect score: 172  
Sequence: 1 USELDDRADALQAXASQPEFXSAKLKRWKGNLK 35

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq.23Sep04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	169	98.3	37	2	AAR6822 VAMP isoc
2	169	98.3	40	4	AAB50301 VAMP2 pep
3	169	98.3	40	4	AAB48582 VAMP2 pep
4	169	98.3	42	5	AA015163 Clostridi
5	169	98.3	54	2	AAB39482 Gene 49 h
6	169	98.3	62	2	AAR6822 VAMP isoc
7	169	98.3	115	7	ADES7598 Human Pro
8	169	98.3	115	7	ADES7612 Rat Prote
9	169	98.3	115	7	ADE60831 Human Pro
10	169	98.3	115	7	ADES7606 Human Pro
11	169	98.3	115	7	ADE60829 Rat Prote
12	169	98.3	115	7	ADES7600 Rat Prote
13	169	98.3	115	7	ADES7604 Rat Prote
14	169	98.3	115	7	ADES7596 Rat Prote
15	169	98.3	115	7	ADES7602 Human Pro
16	169	98.3	115	7	ADES7610 Human Pro
17	169	98.3	115	7	ADES7592 Rat Prote
18	169	98.3	115	7	ADES7594 Human Pro
19	169	98.3	115	7	ADES7614 Human Pro
20	169	98.3	115	7	ADES7608 Rat Prote
21	169	98.3	116	2	AAW30104 Vesicle-a
22	169	98.3	116	2	AAW43425 Rat Vesic
23	169	98.3	116	3	AAV88243 Bovine sy
24	169	98.3	116	5	ABP43681 VAMP-2 se
25	169	98.3	116	6	ABP76220 Human GEN

26 169 98.3 116 6 AAE36664 Aae36664 Human VAM

27 169 98.3 116 7 ABW01719 ABW01719 Bovine VA

28 169 98.3 116 7 ABW01705 ABW01705 Human VAM

29 169 98.3 116 7 ABW01705 ABW01705 Human VAM

30 169 98.3 116 7 ADG89011 ADG89011 Bovine sy

31 169 98.3 116 8 ADM97006 ADM97006 Mouse VAM

32 169 98.3 116 8 ADM97007 ADM97007 Bovine VA

33 169 98.3 116 8 ADM97005 ADM97005 Human VAM

34 169 98.3 368 3 AAY43843 Aay43843 Amino aci

35 169 98.3 368 3 AAY43843 Aay43843 Amino aci

36 169 98.3 608 3 AAY43845 Aay43845 Amino aci

37 169 98.3 609 7 ADF90406 Adf90406 Rat VAMP

38 167 97.1 35 5 AA015157 Aa015157 Clostridi

39 167 97.1 82 3 AAY88244 Aay88244 Xenopus s

40 167 97.1 82 7 ADG89012 ADG89012 Xenopus s

41 167 97.1 114 7 ABW01720 ABW01720 Frog VAMP

42 167 97.1 114 8 ADM97008 ADM97008 Frog VAMP

43 164 95.3 35 2 AAR6824 Aar6824 VAMP isoc

44 164 95.3 100 2 AAW04182 Aaw04182 Celluldyrev

## ALIGNMENTS

RESULT 1  
AAR6822 standard; peptide: 37 AA.

AC AAR6822; (first entry)  
DT 15-AUG-1996  
XX VAMP isoform-1 residues 60-94 (plus N- and C-terminal cysteines).

DE VAMP; vesicle-associated membrane protein; SNRP-25; syntaxin;  
XX VAMP; vesicle-associated membrane protein; SNRP-25; syntaxin;  
KW neurotransmitter; neurotoxin; botulinum; botulinism; cleavage; substrate;  
XX antibody; detection; assay.

OS Synthetic.

PH Key Location/Qualifiers

FT Misc-difference 1 /label= N-terminal Cysteine  
FT /note= "may be present to attach peptide to solid-phase"

FT Peptide 2..36 /note= "VAMP isoform-1 residues 60-94"

FT Misc-difference 37 /label= C-terminal cysteine  
FT /note= "may be present to attach to peptide to solid-phase"

PN WO9533850-A1.

14-DEC-1995.

02-JUN-1995; 95WO-GB001279.

03-JUN-1994; 94GB-00011138.

PA (MICR-) MICROBIOLOGICAL RES AUTHORITY.  
(CAMR-) CAMR CENT APPLIED MICROBIOLOGY & RES.

PI Shore CC, Hallis B, Tames BAF, Quinn CP;

DR WPI; 1996-040249/04.  
XX Assay for botulinum or tetanus toxin - by combining test cpd. with

PT substrate which is cleaved by the toxin, and antibody specific for the

XX cleaved but not uncleaved substrate.  
XX Example 1; Page 28-29; 48pp; English.

CC The botulinum neurotoxins possess highly specific zinc-endopeptidase  
 CC activities within their light sub-units. Depending on the neurotoxin type  
 CC these act to cleave small proteins within the nerve cell which are  
 CC involved in neurotransmitter release. Antibodies are used in assays which  
 CC detect cleaved but not uncleaved substrate. An assay for botulinum type B  
 CC uses the present sequence as a substrate. It is VAMP (vesicle-associated  
 CC membrane protein) isoform-1, residues 60-94. The VAMP peptide can be  
 CC attached by a C- or N-terminal cysteine to a solid phase

XX Sequence 37 AA;

XX Query Match 98.3%; Score 169; DB 2; Length 37;  
 XX Best Local Similarity 94.3%; Pred. No. 6.6e-17;  
 XX Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQXASQFEXSAKLRKRYWNLK 35  
 DB 2 LSELDDRADALQAGASQFETSAKLRKRYWNLK 36

RESULT 2  
 ID AAB50301 standard; peptide; 40 AA.

AC AAB50301;

DT 08-MAR-2001 (first entry)

XX VAMP2 peptide.

KW VAMP2; antibacterial; Botulinum toxin inhibitor; BttxB; previn;  
 KW tetanus neurotoxin; buforin.

OS Unidentified.

XX MO200069891-A2.

PD 23-NOV-2000.

PF 15-MAY-2000; 2000WO-US013215.

PR 17-MAY-1999; 99US-0134446P.

XX (USSA) US DEPT OF THE ARMY.

PA Gordon RK, Moorad DR, Doctor BP, Garcia GE;

DR WPI; 2001-025001/03.

PT Novel Previn compounds useful for inhibiting the protease activity of  
 PT Botulinum B and tetanus toxins.

PS Disclosure; Page 5; 47pp; English.

CC The present sequence was investigated in the search for Botulinum toxin  
 CC inhibitors (BttxB). Previn compounds which inhibit the enzymatic activity  
 CC of BttxB and tetanus neurotoxins were isolated. Previns may be used to  
 CC construct compounds such as buforinins

XX Sequence 40 AA;

XX Query Match 98.3%; Score 169; DB 4; Length 40;  
 XX Best Local Similarity 94.3%; Pred. No. 7.2e-17;  
 XX Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQXASQFEXSAKLRKRYWNLK 35  
 DB 6 LSELDDRADALQAGASQFETSAKLRKRYWNLK 40

RESULT 3  
 ID AAB48582 standard; peptide; 40 AA.

XX AAB48582;

AC 08-MAR-2001 (first entry)

DT VAMP2 peptide.

DE Buforin; Botulinum toxin B; BttxB; Tetanus neurotoxin; endoprotease;

KW antibacterial; VAMP2; synapobrevin.

XX Unidentified.

XX MO200069891-A2.

PD 23-NOV-2000.

PF 11-MAY-2000; 2000WO-US012909.

PR 14-MAY-1999; 99US-0134216P.

XX (USSA) US DEPT OF THE ARMY.

PA Garcia GE, Gordon RK, Moorad DR, Doctor BP;

DR WPI; 2001-102250/11.

PT Novel peptides capable of inhibiting the enzymatic activity of Botulinum  
 PT toxin B, and Tetanus neurotoxins useful for preventing or treating toxic  
 PT poisoning such as Botulinum toxin and tetanus poisoning.

PS Disclosure; Page 5; 47pp; English.

CC The present sequence is one of a number of peptide or peptide-like  
 CC compounds, designated buforins, which inhibit the enzymatic activity of  
 CC Botulinum toxin B (BttxB) and Tetanus neurotoxins. The buforins are  
 CC useful for treating Botulinum or tetanus intoxication by administering a  
 CC composition comprising a buforin to the subject prior to the contact with  
 CC BttxB or tetanus intoxication. Antibodies specific for buforins are  
 CC useful for detecting buforins by forming immunocomplexes. The buforins  
 CC have improved circulatory half-life, solubility, resistance to  
 CC degradation and interaction with the active site of the toxin

XX Sequence 40 AA;

XX Query Match 98.3%; Score 169; DB 4; Length 40;  
 XX Best Local Similarity 94.3%; Pred. No. 7.2e-17;  
 XX Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQXASQFEXSAKLRKRYWNLK 35  
 DB 6 LSELDDRADALQAGASQFETSAKLRKRYWNLK 40

RESULT 4  
 ID AAO15163 standard; peptide; 42 AA.

AC AAO15163;

DT 02-SEP-2002 (first entry)

DE Clostridial neurotoxin protease substrate peptide 2.

XX Clostridial neurotoxin substrate; botulinum neurotoxin substrate; FRET;

KW fluorescence resonant energy transfer assay; quenched-signal;

KW clostridial neurotoxin detection; food.

XX Unidentified.

XX Key Location/Qualifiers  
 XX Modified-site 1 /note= "N-fluoresceinyl-L-glycine"  
 XX Cleavage-site 20..21

/note= "The peptide is cleaved between these two residues  
by the clostridial neurotoxin"

WO200225284-A2.

28-MAR-2002.

25-SEP-2001; 2001WO-US030188.

25-SEP-2000; 2000US-0235050P.

(USME-) US MEDICAL RES INST INFECTIOUS DISEASES.

Schmidt JT, Stafford RG;

WPI; 2002-499829/53.

Substrate useful in e.g. an assay for the protease activity of  
clostridial neurotoxin, comprises modified peptide or protein.

Claim 24; Page 15; 48pp; English.

The invention comprises clostridial neurotoxin substrate peptides which  
can serve as fluorescence resonant energy transfer assay (FRET) or  
quenched-signal substrates in assays for the proteolytic activities of  
clostridial neurotoxins. The invention further comprises clostridium  
botulinum neurotoxin substrate peptides that can serve as immobilised  
substrates (i.e. bound to a solid phase) in assays for the proteolytic  
activities of clostridial neurotoxins. The clostridial (including the  
Clostridium botulinum) neurotoxin substrate peptides are useful for  
detecting the presence of clostridial neurotoxins in a sample (e.g. food  
or an environmental sample). The present amino acid sequence represents a  
clostridial neurotoxin substrate peptide of the invention

Sequence 42 AA;

Query Match 98.3%; Score 169; DB 5; Length 42;  
Best Local Similarity 94.3%; Pred. No. 7.6e-17;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDPRADALQAXASQFEXSAKLKRYWKXK 35  
DB 4 LSELDPRADALQAGASQFETSAAKLKRYWKXK 38

RESULT 5  
AAB39482 ID AAB39482 standard; protein; 54 AA.

AC AAB39482;

DT 02-FEB-2001 (first entry)

DE Gene 49 human secreted protein homologous amino acid sequence #111.

Human; secreted protein; diagnosis; cytostatic; immunosuppressive;  
neurotropic; neuroprotection; antiviral; antiallergic; hepatotropic;  
antidiabetic; antiinflammatory; antitumor; anticonvulsant;  
antibacterial; antifungal; antiparasitic; cardiac; gene therapy;  
food additive; preservative; chromosome identification; cancer;  
female reproductive system disorder; immune disorder; wound healing;  
cardiovascular disorder; neurological disease; infectious disease;  
infection.

OS Bos taurus.

PN WO200058340-A2.

PD 05-OCT-2000.

PF 23-MAR-2000; 2000WO-US007724.

PR 26-MAR-1999; 99US-0126510P

PR 07-JAN-2000; 2000US-0174850P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Ruben SM, Komatsu G;

WPI; 2000-594638/56.

Fifty nucleic acid molecules encoding human secreted proteins, useful in  
the prevention, treatment and diagnosis of cancer, immune disorders,  
cardiovascular disorders and neurological diseases.

Disclosure; Page 390; 391pp; English.

The polynucleotide sequences given in AAC74337 to AAC74386 encode the  
human secreted proteins given in AAB39402 to AAB39451. AAB39452 to  
AAB39484 represent human secreted polypeptide sequences and proteins  
homologous to them, which are given in the exemplification of the present  
invention. Human secreted proteins have activities based on the tissues  
and cells the genes are expressed in. Example of activities include:  
cytostatic; immunosuppressive; neurotropic; neuroprotective; antiviral;  
antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;  
antibacterial; antiparasitic; antifungal; antiparasitic; and  
cardiac. The polynucleotides and polypeptides are useful for preventing,  
treating or ameliorating a medical condition in e.g. humans, mice,  
rabbits, goats, horses, cats, dogs, chickens or sheep. The polypeptides  
can also be used as a food additive or preservative to increase or  
decrease storage capabilities. The polynucleotide are useful for  
chromosome identification. They are also useful as probes for diagnosing  
a disorder related to the female reproductive system, particularly breast  
and/or ovarian cancer. They are also useful in the gene therapy of breast  
and ovarian cancer. Secreted protein nucleic acids, proteins, antibodies,  
agonists and antagonists are useful in the diagnosis, treatment and  
prevention of: (a) cancer; (b) immune disorders; (c) cardiovascular  
disorders; (d) wound healing; (e) neurological diseases; and (f)  
infectious diseases such as viral, bacterial, fungal and parasitic  
infections. AAC74328 to AAC74336 and AAB39401 represent sequences used in  
the exemplification of the present invention

Sequence 54 AA;

Query Match 98.3%; Score 169; DB 3; Length 54;  
Best Local Similarity 94.3%; Pred. No. 1e-16;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDPRADALQAXASQFEXSAKLKRYWKXK 35  
DB 20 LSELDPRADALQAGASQFETSAAKLKRYWKXK 54

RESULT 6  
AAB6821 ID AAB6821 standard; peptide; 62 AA.

AC AAB6821;

DT 15-AUG-1996 (first entry)

DE VAMP isoform-1 residues 33-94.

VAMP, vesicle-associated membrane protein; SNAP-25; syntaxin;  
neurotransmitter; neurotoxin; botulinum; botulinum; cleavage; substrate;  
antibody; detection; assay.

OS Synthetic.

PN WO9533850-A1.

PD 14-DEC-1995.

PF 02-JUN-1995; 95WO-GB001279.

PR 03-JUN-1994; 94GB-00011138.

XX (MIGR-) MICROBIOLOGICAL RES AUTHORITY.  
PA (CAMR-) CAMR CENT APPLIED MICROBIOLOGY & RES.  
XX  
XX  
PI Shone CC, Hallis B, James BAF, Quinn CP;  
DR WPI; 1996-040249/04.  
XX  
PT Assay for botulinum or tetanus toxin - by combining test cpd. with  
PT substrate which is cleaved by the toxin, and antibody specific for the  
PT cleaved but not uncleaved substrate.  
XX  
PS Example 3; Page 28; 48pp; English.  
XX The botulinum neurotoxins possess highly specific zinc-endopeptidase  
CC activities within their light sub-units. Depending on the neurotoxin type  
CC these act to cleave small proteins within the nerve cell which are  
CC involved in neurotransmitter release. Antibodies are used in assays which  
CC detect cleaved but not uncleaved substrate. Tetanus toxin cleaves the  
CC protein VAMP (vesicle-associated membrane protein) at an identical site  
CC to that of botulinum toxin type B (BONT/B). The specificities of the  
CC endopeptidase activities of the two toxins however differ in the minimum  
CC peptide substrate size required for cleavage. While BONT/B requires  
CC peptide substrates of 30-35 residues in length for optimal cleavage, the  
CC requirement for tetanus toxin is peptide substrates of >50 residues in  
CC length. The present sequence, VAMP isoform-1 residues 33-94, is a  
CC suitable substrate for tetanus toxin  
XX  
SQ Sequence 62 AA;  
Query Match 98.3%; Score 169; DB 2; Length 62;  
Best Local Similarity 94.3%; Pred. No. 1.2e-16;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 LSELDPRADALQXASQFEXSAKLRKRYWKNLK 35  
DB 28 LSELDPRADALQAGASQFESSAAKLRKRYWKNLK 62  
RESULT 7  
ID ADE57598 standard; protein; 115 AA.  
AC ADE57598;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Human Protein P19065, SEQ ID NO 3460.  
XX  
KW Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SN1; Chung.  
XX  
OS Homo sapiens.  
XX  
PN WO2003016475-A2.  
XX  
PD 27-FEB-2003.  
XX  
PF 14-AUG-2002; 2002WO-US025765.  
XX  
PR 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
XX  
PI Woolf C, D'urso D, Befort K, Costigan M;  
DR WPI; 2003-268312/26.  
DR GENBANK; P19065.  
XX

PT New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
XX  
XX Claim 1; Page; 1017pp; English.  
XX  
CC The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (SN1), chronic constriction  
CC injury (CCI) and spared nerve injury (SN1)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 115 AA;  
Query Match 98.3%; Score 169; DB 7; Length 115;  
Best Local Similarity 94.3%; Pred. No. 2.3e-16;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 LSELDPRADALQXASQFEXSAKLRKRYWKNLK 35  
DB 59 LSELDPRADALQAGASQFETSAAKLRKRYWKNLK 93  
RESULT 8  
ID ADE57612 standard; protein; 115 AA.  
AC ADE57612;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Rat Protein Q64357, SEQ ID NO 3474.  
XX  
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
KW chronic constriction injury; CCI; spared nerve injury; SN1; Chung.  
XX  
OS Rattus norvegicus.  
XX  
PN WO2003016475-A2.  
XX  
PD 27-FEB-2003.  
XX  
PF 14-AUG-2002; 2002WO-US025765.  
XX  
PR 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX  
PA (GEHO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
XX  
PI Woolf C, D'urso D, Befort K, Costigan M;  
XX



XX WPI, 2003-268312/26.  
DR GENBANK; Q64357.

XX New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.

XX Claim 1, Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 115 AA;

Query Match 98.3%; Score 169; DB 7; Length 115;  
Best Local Similarity 94.3%; Pred. No. 2,3e-16;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDPRADALQAXASQPEXSAKLKRYKWWKLNK 35  
Db 59 LSELDPRADALQAGASQFETSAKLKRYKWWKLNK 93

RESULT 9  
ADE60831  
ID ADE60831 standard; protein; 115 AA.

XX ADE60831;

XX 29-JAN-2004 (first entry)

XX Human Protein P19065, SEQ ID NO 6743.

XX Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.

XX Homo sapiens.

XX WO2003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

XX 01-NOV-2001; 2001US-0346382P.

XX 26-NOV-2001; 2001US-0333347P.

XX (GENO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.

XX Woolf C, D'urso D, Belfort K, Costigan M;

XX WPI; 2003-268312/26.

XX GENBANK; P19065.

XX New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.

XX Claim 1, Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 115 AA;

Query Match 98.3%; Score 169; DB 7; Length 115;  
Best Local Similarity 94.3%; Pred. No. 2,3e-16;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDPRADALQAXASQPEXSAKLKRYKWWKLNK 35  
Db 59 LSELDPRADALQAGASQFETSAKLKRYKWWKLNK 93

RESULT 10  
ADE57606  
ID ADE57606 standard; protein; 115 AA.

XX ADE57606;

XX 29-JAN-2004 (first entry)

XX Human Protein P19065, SEQ ID NO 3468.

XX Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.

XX Homo sapiens.

XX WO2003016475-A2.

XX 27-FEB-2003.

PF 14-AUG-2002; 2002WO-US025765.  
XX 14-AUG-2001; 2001US-0312147P.  
XX 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX  
XX (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX  
XX Woolf C, D'urso D, Befort K, Costigan M;  
PI WPI; 2003-268312/26.  
DR GENBANK; P19065.  
XX  
XX New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
XX  
XX Claim 1; Page; 1017pp; English.  
XX  
XX The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (shown in table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pcr\_sequences.  
XX  
XX Sequence 115 AA;  
SQ

Query Match 98.3%; Score 169; DB 7; Length 115;  
Best Local Similarity 94.3%; Pred. No. 2.3e-16;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQXASQFEXSAKLRKRYWKNLK 35  
DB 59 LSELDDRADALQXASQFETSAAKLRKRYWKNLK 93

RESULT 11  
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XX  
XX ADE60829;  
AC  
XX 29-JAN-2004 (first entry)  
DT  
XX  
XX Rat Proein Q64357, SEQ ID NO 6741.  
DE  
XX  
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
KM chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
XX  
XX Ratus norvegicus.  
OS  
XX

PN W02003016475-A2.  
XX  
XX 27-FEB-2003.  
XX  
XX 14-AUG-2002; 2002WO-US025765.  
PF  
XX  
XX 14-AUG-2001; 2001US-0312147P.  
XX 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX  
XX (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX  
XX Woolf C, D'urso D, Befort K, Costigan M;  
PI WPI; 2003-268312/26.  
DR GENBANK; Q64357.  
XX  
XX New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
XX  
XX Claim 1; Page; 1017pp; English.  
XX  
XX The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a rat protein (shown in table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pcr\_sequences.  
XX  
XX Sequence 115 AA;  
SQ

Query Match 98.3%; Score 169; DB 7; Length 115;  
Best Local Similarity 94.3%; Pred. No. 2.3e-16;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQXASQFEXSAKLRKRYWKNLK 35  
DB 59 LSELDDRADALQXASQFETSAAKLRKRYWKNLK 93

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ID ADE57600 standard; protein; 115 AA.  
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AC  
XX 29-JAN-2004 (first entry)  
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XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
KM

KM chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
 XX Rattus norvegicus.  
 OS WO2003016475-A2.  
 PN 27-FEB-2003.  
 PD 14-AUG-2002; 2002WO-US025765.  
 XX 14-AUG-2001; 2001US-0312147P.  
 PR 01-NOV-2001; 2001US-0346382P.  
 XX 26-NOV-2001; 2001US-0333347P.  
 PA (GEHO) GEN HOSPITAL CORP.  
 XX (FARB) BAYER AG.  
 PI Woolf C, D'urso D, Befort K, Costigan M;  
 XX WPI; 2003-268312/26.  
 DR GENBANK; Q64357.  
 PT New composition comprising two or more isolated polypeptides, useful for  
 PT preparing a medicament for treating pain in an animal.  
 PS Claim 1; Page; 1017p; English.  
 XX The invention discloses a composition comprising two or more isolated rat  
 CC or human polynucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC claimed are a vector comprising the novel polynucleotide, a host cell  
 CC comprising the vector, a method for identifying a nucleotide sequence  
 CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying an agent  
 CC that increases or decreases the expression of the polynucleotide sequence  
 CC that is differentially expressed in neuronal tissue of a first animal  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
 CC the specification) which is differentially expressed during pain. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 CC  
 CC Sequence 115 AA:  
 SO  
 Query Match 98.3%; Score 169; DB 7; Length 115;  
 Best Local Similarity 94.3%; Pred. No. 2.3e-16;  
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 OY 1 LSEIDRRADALQAXASQFEXSAKLRKRYWKNLK 35  
 DB 59 LSEIDRRADALQAGASQFETSAKLRKRYWKNLK 93  
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 XX ADE57604;  
 AC  
 XX 29-JAN-2004 (first entry)

XX Rat Protein Q64357, SEQ ID NO 3466.  
 DE Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
 XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
 KM Rattus norvegicus.  
 OS WO2003016475-A2.  
 PN 27-FEB-2003.  
 PD 14-AUG-2002; 2002WO-US025765.  
 XX 14-AUG-2001; 2001US-0312147P.  
 PR 01-NOV-2001; 2001US-0346382P.  
 XX 26-NOV-2001; 2001US-0333347P.  
 PA (GEHO) GEN HOSPITAL CORP.  
 XX (FARB) BAYER AG.  
 PI Woolf C, D'urso D, Befort K, Costigan M;  
 XX WPI; 2003-268312/26.  
 DR GENBANK; Q64357.  
 PT New composition comprising two or more isolated polypeptides, useful for  
 PT preparing a medicament for treating pain in an animal.  
 PS Claim 1; Page; 1017p; English.  
 XX The invention discloses a composition comprising two or more isolated rat  
 CC or human polynucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC claimed are a vector comprising the novel polynucleotide, a host cell  
 CC comprising the vector, a method for identifying a nucleotide sequence  
 CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying an agent  
 CC that increases or decreases the expression of the polynucleotide sequence  
 CC that is differentially expressed in neuronal tissue of a first animal  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
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 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
 CC the specification) which is differentially expressed during pain. Note:  
 CC The sequence data for this patent did not form part of the printed  
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 DB 59 LSEIDRRADALQAGASQFETSAKLRKRYWKNLK 93  
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 XX ADE57596

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XX AC ADE57596;
XX AC 29-JAN-2004 (first entry)
XX DT Rat Protein Q64357, SEQ ID NO 3458.
XX DE
XX DE Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;
XX DE chronic constriction injury; CCI; spared nerve injury; SNI; Chung.
XX OS Rattus norvegicus.
XX PN WO2003016475-A2.
XX PD 27-FEB-2003.
XX PF 14-AUG-2002; 2002WO-US025765.
XX PR 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX PA (GEHO ) GEN HOSPITAL CORP.
XX PA (FARB ) BAYER AG.
XX PI Woolf C, D'urso D, Befort K, Costigan M;
XX DR WPI; 2003-268312/26.
XX DR GENBANK; Q64357.
XX PT
XX PT New composition comprising two or more isolated polypeptides, useful for
XX PS preparing a medicament for treating pain in an animal.
XX PS Claim 1; Page; 1017p; English.
XX CC The invention discloses a composition comprising two or more isolated rat
XX CC or human polynucleotides or a polynucleotide which represents a fragment,
XX CC derivative or allelic variation of the nucleic acid sequence. Also
XX CC claimed are a vector comprising the novel polynucleotide, a host cell
XX CC comprising the vector, a method for identifying a nucleotide sequence
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XX CC kit to perform the method, an array, a method for identifying an agent
XX CC that increases or decreases the expression of the polynucleotide sequence
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XX CC subjected to pain, a method for identifying a compound which regulates
XX CC the expression of a polynucleotide sequence which is differentially
XX CC expressed in an animal subjected to pain, a method for identifying a
XX CC compound that regulates the activity of one or more of the
XX CC polynucleotides, a method for producing a pharmaceutical composition, a
XX CC method for identifying a compound or small molecule that regulates the
XX CC activity in an animal of one or more of the polypeptides given in the
XX CC specification, a method for identifying a compound useful in treating
XX CC pain and a pharmaceutical composition comprising the one or more
XX CC polypeptides or their antibodies. The polynucleotide or the compound that
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XX CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction
XX CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene
XX CC therapy). The sequence presented is a rat protein (shown in Table 2 of
XX CC the specification) which is differentially expressed during pain. Note:
XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic form directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 115 AA;
XX
XX Query Match 98.3%; Score 169; DB 7; Length 115;
XX Best Local Similarity 94.3%; Pred. No. 2,3e-16;
XX Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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XX ID ADE57602;
XX AC ADE57602;
XX DT 29-JAN-2004 (first entry)
XX DE Human Protein P19065, SEQ ID NO 3464.
XX DE
XX DE Human; pain; neuronal tissue; gene therapy;
XX DE spinal segmental nerve injury; chronic constriction injury; CCI;
XX DE spared nerve injury; SNI; Chung.
XX OS Homo sapiens.
XX PN WO2003016475-A2.
XX PD 27-FEB-2003.
XX PF 14-AUG-2002; 2002WO-US025765.
XX PR 14-AUG-2001; 2001US-0312147P.
XX PR 01-NOV-2001; 2001US-0346382P.
XX PR 26-NOV-2001; 2001US-0333347P.
XX PA (GEHO ) GEN HOSPITAL CORP.
XX PA (FARB ) BAYER AG.
XX PI Woolf C, D'urso D, Befort K, Costigan M;
XX DR WPI; 2003-268312/26.
XX DR GENBANK; P19065.
XX PT
XX PT New composition comprising two or more isolated polypeptides, useful for
XX PS preparing a medicament for treating pain in an animal.
XX PS Claim 1; Page; 1017p; English.
XX CC The invention discloses a composition comprising two or more isolated rat
XX CC or human polynucleotides or a polynucleotide which represents a fragment,
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XX CC that increases or decreases the expression of the polynucleotide sequence
XX CC that is differentially expressed in neuronal tissue of a first animal
XX CC subjected to pain, a method for identifying a compound which regulates
XX CC the expression of a polynucleotide sequence which is differentially
XX CC expressed in an animal subjected to pain, a method for identifying a
XX CC compound that regulates the activity of one or more of the
XX CC polynucleotides, a method for producing a pharmaceutical composition, a
XX CC method for identifying a compound or small molecule that regulates the
XX CC activity in an animal of one or more of the polypeptides given in the
XX CC specification, a method for identifying a compound useful in treating
XX CC pain and a pharmaceutical composition comprising the one or more
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XX CC the specification) which is differentially expressed during pain. Note:
XX CC The sequence data for this patent did not form part of the printed
XX CC specification, but was obtained in electronic form directly from WIPO at
XX CC ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 115 AA;
XX
XX Query Match 98.3%; Score 169; DB 7; Length 115;
XX Best Local Similarity 94.3%; Pred. No. 2,3e-16;
XX Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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✓ Tue Nov 2 10:45:11 2004

us-10-802-574-3.rag

Page 9

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Db	59	ISELDDRADALQAGASQFETSAKLKRYWKNLK	93

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Job time : 92 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 1, 2004, 17:53:05 ; Search time 23.4375 Seconds  
(without alignments)  
99.035 Million cell updates/sec

Title: US-10-802-574-3  
Perfect score: 172  
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Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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3	169	98.3	35	3	US-08-015-960-9
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6	169	98.3	35	3	US-09-534-572-11
7	169	98.3	40	4	US-09-570-022-16
8	169	98.3	40	4	US-09-570-023-8
9	169	98.3	42	4	US-09-962-3608-9
10	169	98.3	62	2	US-08-760-001-8
11	169	98.3	62	2	US-09-015-960-8
12	169	98.3	62	3	US-08-534-572-8
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15	169	98.3	116	1	US-08-393-985-16
16	169	98.3	116	3	US-08-621-018B-10
17	169	98.3	116	3	US-08-819-286-2
18	169	98.3	116	4	US-09-483-665-10
19	169	98.3	35	4	US-09-962-3608-3
20	169	97.1	82	4	US-08-621-018B-11
21	167	97.1	82	4	US-08-483-665-11
22	164	95.3	100	4	US-08-621-018B-6
23	164	95.3	100	4	US-09-483-665-6
24	164	95.3	103	1	US-08-409-373B-3
25	164	95.3	103	1	US-08-409-373B-3
26	164	95.3	103	3	US-08-621-018B-9
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29	164	95.3	347	4	US-09-430-656-30	Sequence 30, Appl
30	164	95.3	350	4	US-09-513-783A-30	Sequence 30, Appl
31	164	95.3	350	4	US-09-430-656-28	Sequence 28, Appl
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33	157	91.3	118	1	US-08-393-985-14	Sequence 14, Appl
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42	81	47.1	20	3	US-08-819-286-13	Sequence 8, Appl
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## ALIGNMENTS

RESULT 1  
US-08-760-001-9  
Sequence 9, Application US/08760001  
Patent No. 5962637  
GENERAL INFORMATION:  
APPLICANT: Shone, Clifford C.  
APPLICANT: Hallis, Bassam  
APPLICANT: James, Benjamin A. F.  
APPLICANT: Quinn, Conrad P.  
TITLE OF INVENTION: TOXIN ASSAY  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
ADDRESS: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/760,001  
FILING DATE: Herewith  
CLASSIFICATION: 530  
PRIORITY APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB95/01279  
FILING DATE: 02-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32, 893  
REFERENCE/DOCKET NUMBER: 1581.0120001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2543  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-760-001-9  
Query Match 98.3%; Score 169; DB 2; Length 35;  
Best Local Similarity 94.3%; Pred. No. 66-18;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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1 LSELDDRADALQAGASQFESSAKLRKRYWNLK 35

Db 1 LSELDDRADALQAGASQFESSAKLRKRYWNLK 35

RESULT 2  
US-08-760-001-11  
Sequence 11, Application US/08760001  
Patent No. 5962637  
GENERAL INFORMATION:  
APPLICANT: Shone, Clifford C.  
APPLICANT: Hallie, Bassam  
APPLICANT: James, Benjamin A. F.  
APPLICANT: Quinn, Conrad P.  
TITLE OF INVENTION: TOXIN ASSAY  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/760,001  
FILING DATE: Herewith  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB95/01279  
FILING DATE: 02-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32, 893  
REFERENCE/DOCKET NUMBER: 1581.0120001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2543  
TELEFAX: 202-371-2543  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-760-001-11

Query Match 98.3%; Score 169; DB 2; Length 35;  
Best Local Similarity 94.3%; Pred. No. 6e-18;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAXASQFEXSAKLRKRYWNLK 35  
1 LSELDDRADALQAGASQFESSAKLRKRYWNLK 35

Db 1 LSELDDRADALQAGASQFESSAKLRKRYWNLK 35

RESULT 3  
US-09-015-960-9  
Sequence 9, Application US/09015960  
Patent No. 6043042  
GENERAL INFORMATION:  
APPLICANT: Shone, Clifford C.  
APPLICANT: Hallie, Bassam  
APPLICANT: James, Benjamin A. F.  
APPLICANT: Quinn, Conrad P.  
TITLE OF INVENTION: TOXIN ASSAY  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/015,960  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/760,001  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32, 893  
REFERENCE/DOCKET NUMBER: 1581.0120001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2543  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-015-960-9

Query Match 98.3%; Score 169; DB 3; Length 35;  
Best Local Similarity 94.3%; Pred. No. 6e-18;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAXASQFEXSAKLRKRYWNLK 35  
1 LSELDDRADALQAGASQFESSAKLRKRYWNLK 35

Db 1 LSELDDRADALQAGASQFESSAKLRKRYWNLK 35

RESULT 4  
US-09-015-960-11  
Sequence 11, Application US/09015960  
Patent No. 6043042  
GENERAL INFORMATION:  
APPLICANT: Shone, Clifford C.  
APPLICANT: Hallie, Bassam  
APPLICANT: James, Benjamin A. F.  
APPLICANT: Quinn, Conrad P.  
TITLE OF INVENTION: TOXIN ASSAY  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/015,960  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/760,001  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:



NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1581.0120001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2543  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-015-960-11

Query Match 98.3%; Score 169; DB 3; Length 35;  
Best Local Similarity 94.3%; Pred. No. 66-18;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAXASQFESAAKLKRYWKNLK 35  
Db 1 LSELDDRADALQAGASQFESAAKLKRYWKNLK 35

## RESULT 5

US-09-534-572-9  
Sequence 9, Application US/09534572  
Patent No. 6337386  
GENERAL INFORMATION:  
APPLICANT: Shore, Clifford C.  
APPLICANT: Hallis, Bassam  
APPLICANT: James, Benjamin A. F.  
APPLICANT: Quinn, Conrad P.  
TITLE OF INVENTION: TOXIN ASSAY  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/534,572  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/015,960  
FILING DATE: 30-JAN-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/760,001  
FILING DATE: 30-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB95/01279  
FILING DATE: 02-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1581.0120003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2543  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: peptide  
US-09-534-572-9

Query Match 98.3%; Score 169; DB 3; Length 35;  
Best Local Similarity 94.3%; Pred. No. 66-18;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAXASQFESAAKLKRYWKNLK 35  
Db 1 LSELDDRADALQAGASQFESAAKLKRYWKNLK 35

## RESULT 6

US-09-534-572-11  
Sequence 11, Application US/09534572  
Patent No. 6337386  
GENERAL INFORMATION:  
APPLICANT: Shore, Clifford C.  
APPLICANT: Hallis, Bassam  
APPLICANT: James, Benjamin A. F.  
APPLICANT: Quinn, Conrad P.  
TITLE OF INVENTION: TOXIN ASSAY  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/534,572  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/015,960  
FILING DATE: 30-JAN-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/760,001  
FILING DATE: 30-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB95/01279  
FILING DATE: 02-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1581.0120003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2543  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-534-572-11

Query Match 98.3%; Score 169; DB 3; Length 35;  
Best Local Similarity 94.3%; Pred. No. 66-18;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDDRADALQAXASQFESAAKLKRYWKNLK 35  
Db 1 LSELDDRADALQAGASQFESAAKLKRYWKNLK 35

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RESULT 7
US-09-570-022-16
; Sequence 16, Application US/09570022
; Patent No. 6573244
; GENERAL INFORMATION:
; APPLICANT: GORDON, RICHARD K.
; APPLICANT: MOORAD, DEBORAH R.
; APPLICANT: DOCTOR, BHUPENDRA P.
; APPLICANT: GARCIA, GREGORY E.
; TITLE OF INVENTION: PREVIOUS AS SPECIFIC INHIBITORS AND THERAPEUTIC AGENTS
; TITLE OF INVENTION: FOR BOTULINUM TOXIN B AND TETANUS NEUROTOXINS
; FILE REFERENCE: 38644-17051
; CURRENT APPLICATION NUMBER: US/09/570,022
; CURRENT FILING DATE: 2000-05-12
; PRIOR APPLICATION NUMBER: 60/134,446
; PRIOR FILING DATE: 1999-05-17
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 16
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-570-022-16

Query Match          98.3%; Score 169; DB 4; Length 40;
Best Local Similarity 94.3%; Pred. No. 7e-18; 2; Indels 0; Gaps 0;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAXASQFEXSAKLRKRYWKNLK 35
    |||||
    6 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 40
    |||||

RESULT 8
US-09-570-023-8
; Sequence 8, Application US/09570023
; Patent No. 6713444
; GENERAL INFORMATION:
; APPLICANT: GARCIA, GREGORY E.
; APPLICANT: MOORAD, RICHARD K.
; APPLICANT: DOCTOR, DEBBIE R.
; APPLICANT: MOORAD, BHUPENDRA P.
; TITLE OF INVENTION: BUPORIN I AS A SPECIFIC INHIBITOR AND THERAPEUTIC AGENT
; TITLE OF INVENTION: FOR BOTULINUM TOXIN B AND TETANUS NEUROTOXINS
; FILE REFERENCE: 37833-20004.00
; CURRENT APPLICATION NUMBER: US/09/570,023
; CURRENT FILING DATE: 2000-05-12
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 8
; LENGTH: 40
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-570-023-8

Query Match          98.3%; Score 169; DB 4; Length 40;
Best Local Similarity 94.3%; Pred. No. 7e-18; 2; Indels 0; Gaps 0;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAXASQFEXSAKLRKRYWKNLK 35
    |||||
    6 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 40
    |||||

RESULT 9
US-09-962-360B-9
; Sequence 9, Application US/09962360B
; Patent No. 6762280
; GENERAL INFORMATION:
; /9

APPLICANT: Schmidt, James J.
APPLICANT: Stafford, Robert G.
TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi
TITLE OF INVENTION: Neurotoxins
FILE REFERENCE: 003/224/SAP
CURRENT APPLICATION NUMBER: US/09/962,360B
CURRENT FILING DATE: 2002-08-19
PRIOR APPLICATION NUMBER: US 60/235,050
PRIOR FILING DATE: 2001-09-25
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 9
LENGTH: 42
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BONT B
NAME/KEY: misc_feature
LOCATION: 1
OTHER INFORMATION: Xaa at 1 is N-fluoresceinyl-glycine
US-09-962-360B-9

Query Match          98.3%; Score 169; DB 4; Length 42;
Best Local Similarity 94.3%; Pred. No. 7.4e-18;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAXASQFEXSAKLRKRYWKNLK 35
    |||||
    4 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 38
    |||||

RESULT 10
US-08-760-001-8
; Sequence 8, Application US/08760001
; Patent No. 5962637
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford C.
; APPLICANT: Hallis, Bassam
; APPLICANT: James, Benjamin A. F.
; APPLICANT: Quinn, Conrad P.
; TITLE OF INVENTION: TOXIN ASSAY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.
; STREET: 1100 New York Ave., N.W., Suite 600
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-3934
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/760,001
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/GB95/01279
; FILING DATE: 02-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Esmond, Robert W.
; REGISTRATION NUMBER: 32,893
; REFERENCE/DOCKET NUMBER: 1581.0120001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2543
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 62 amino acids
; TYPE: amino acid
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STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-760-001-8

Query Match 98.3%; Score 169; DB 2; Length 62;  
Best Local Similarity 94.3%; Pred. No. 1,1e-17;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASQFESSAAKLKRYKWKNLK 35  
DB 28 LSELDDRADALQAGASQFESSAAKLKRYKWKNLK 62

RESULT 11  
US-09-015-960-8  
Sequence 8, Application US/09015960  
Patent No. 6043042  
GENERAL INFORMATION:  
APPLICANT: Shone, Clifford C.  
APPLICANT: Hallis, Bassam  
APPLICANT: James, Benjamin A. F.  
APPLICANT: Quinn, Conrad P.  
TITLE OF INVENTION: TOXIN ASSAY  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/015,960  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/760,001  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Bsmoud, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1581.0120001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2543  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 62 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-015-960-8

Query Match 98.3%; Score 169; DB 3; Length 62;  
Best Local Similarity 94.3%; Pred. No. 1,1e-17;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASQFESSAAKLKRYKWKNLK 35  
DB 28 LSELDDRADALQAGASQFESSAAKLKRYKWKNLK 62

RESULT 12  
US-09-534-572-8  
Sequence 8, Application US/09534572  
Patent No. 6337386

GENERAL INFORMATION:  
APPLICANT: Shone, Clifford C.  
APPLICANT: Hallis, Bassam  
APPLICANT: James, Benjamin A. F.  
APPLICANT: Quinn, Conrad P.  
TITLE OF INVENTION: TOXIN ASSAY  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/534,572  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/015,960  
FILING DATE: 30-JAN-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/760,001  
FILING DATE: 30-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB95/01279  
FILING DATE: 02-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Bsmoud, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1581.0120003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2543  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 62 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-534-572-8

Query Match 98.3%; Score 169; DB 3; Length 62;  
Best Local Similarity 94.3%; Pred. No. 1,1e-17;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASQFESSAAKLKRYKWKNLK 35  
DB 28 LSELDDRADALQAGASQFESSAAKLKRYKWKNLK 62

RESULT 13  
US-08-409-373B-4  
Sequence 4, Application US/08409373B  
Patent No. 5585240  
GENERAL INFORMATION:  
APPLICANT: Stuart, Susan G.  
APPLICANT: Hallis, Phillip R.  
APPLICANT: Sellhamer, Jeffrey J.  
TITLE OF INVENTION: CELLUBREVIN HOMOLOG  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.

ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/409,373B  
FILING DATE: 23-MAR-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0029 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 116 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: X76199  
US-08-409-373B-4

Query Match 98.3%; Score 169; DB 1; Length 116;  
Best Local Similarity 94.3%; Pred. No. 2,3e-17;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAXASQFEXSAKLKRYKWMNLK 35  
DB 60 LSELDDRADALQAGASQFETSAAKLKRYKWMNLK 94

RESULT 14  
US-08-409-373B-4  
Sequence 4, Application US/08409373B  
Patent No. 5650280  
Patent No. 5650280 5585240  
GENERAL INFORMATION:  
APPLICANT: Stuart, Susan G.  
APPLICANT: Sellmeyer, Jeffrey J.  
TITLE OF INVENTION: CELLULREVIN HOMOLOG  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/409,373B  
FILING DATE: 23-MAR-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0029 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:  
LENGTH: 116 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: X76199  
US-08-409-373B-4

Query Match 98.3%; Score 169; DB 1; Length 116;  
Best Local Similarity 94.3%; Pred. No. 2,3e-17;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAXASQFEXSAKLKRYKWMNLK 35  
DB 60 LSELDDRADALQAGASQFETSAAKLKRYKWMNLK 94

RESULT 15  
US-08-393-985-16  
Sequence 16, Application US/08393985  
Patent No. 5693476  
GENERAL INFORMATION:  
APPLICANT: Scheller, Richard H.  
TITLE OF INVENTION: Methods and Compositions for Modulation  
of Vesicular Release  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: 350 Cambridge Avenue, Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/393,985  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Sholtz, Charles K.  
REGISTRATION NUMBER: 38,615  
REFERENCE/DOCKET NUMBER: 8600-0152  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 116 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-393-985-16

Query Match 98.3%; Score 169; DB 1; Length 116;  
Best Local Similarity 94.3%; Pred. No. 2,3e-17;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAXASQFEXSAKLKRYKWMNLK 35  
DB 60 LSELDDRADALQAGASQFETSAAKLKRYKWMNLK 94

Search completed: November 1, 2004, 18:19:41  
Job time : 24.4375 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 1, 2004, 17:59:20 ; Search time 69.0625 Seconds  
(without alignments)  
164,308 Million cell updates/sec

Title: US-10-802-574-3  
Sequence: 1 LSELDRADALQXASQFEXSAKLRKYWKXNK 35

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:\*  
1: /cgn2\_6/prodata/2/pubppa/US07\_PUBCOMB.pep:\*  
2: /cgn2\_6/prodata/2/pubppa/PCF\_NEW\_PUB.pep:\*  
3: /cgn2\_6/prodata/2/pubppa/US06\_NEW\_PUB.pep:\*  
4: /cgn2\_6/prodata/2/pubppa/US07\_NEW\_PUB.pep:\*  
5: /cgn2\_6/prodata/2/pubppa/US08\_NEW\_PUB.pep:\*  
6: /cgn2\_6/prodata/2/pubppa/US08\_NEW\_PUB.pep:\*  
7: /cgn2\_6/prodata/2/pubppa/US08\_PUBCOMB.pep:\*  
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9: /cgn2\_6/prodata/2/pubppa/US09\_PUBCOMB.pep:\*  
10: /cgn2\_6/prodata/2/pubppa/US09\_PUBCOMB.pep:\*  
11: /cgn2\_6/prodata/2/pubppa/US09\_PUBCOMB.pep:\*  
12: /cgn2\_6/prodata/2/pubppa/US10\_PUBCOMB.pep:\*  
13: /cgn2\_6/prodata/2/pubppa/US10\_PUBCOMB.pep:\*  
14: /cgn2\_6/prodata/2/pubppa/US10\_PUBCOMB.pep:\*  
15: /cgn2\_6/prodata/2/pubppa/US10\_PUBCOMB.pep:\*  
16: /cgn2\_6/prodata/2/pubppa/US10\_PUBCOMB.pep:\*  
17: /cgn2\_6/prodata/2/pubppa/US10\_PUBCOMB.pep:\*  
18: /cgn2\_6/prodata/2/pubppa/US10\_PUBCOMB.pep:\*  
19: /cgn2\_6/prodata/2/pubppa/US60\_NEW\_PUB.pep:\*  
20: /cgn2\_6/prodata/2/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result	No.	Score	Match	Length	ID	Description
1	169	98.3	42	10	US-09-962-360B-9	Sequence 9, Appl1
2	169	98.3	116	10	US-09-942-024-4	Sequence 4, Appl1
3	169	98.3	116	10	US-09-942-024-17	Sequence 17, Appl1
4	169	98.3	116	10	US-09-942-024-18	Sequence 18, Appl1
5	169	98.3	116	10	US-09-942-024-4	Sequence 4, Appl1
6	169	98.3	116	10	US-09-942-024-17	Sequence 17, Appl1
7	169	98.3	116	10	US-09-942-024-18	Sequence 18, Appl1
8	169	98.3	116	14	US-10-357-028-10	Sequence 10, Appl1
9	169	98.3	116	15	US-10-261-161-11	Sequence 11, Appl1
10	169	98.3	116	15	US-10-261-161-12	Sequence 12, Appl1
11	169	98.3	116	15	US-10-261-161-13	Sequence 13, Appl1
12	169	98.3	607	10	US-09-293-670-55	Sequence 55, Appl1
13	168	97.7	35	10	US-09-962-360B-3	Sequence 3, Appl1

14	167	97.1	82	14	US-10-357-028-11	Sequence 11, Appl1
15	167	97.1	114	10	US-09-942-024-19	Sequence 19, Appl1
16	167	97.1	114	10	US-09-942-024-19	Sequence 19, Appl1
17	167	97.1	114	15	US-10-261-161-14	Sequence 14, Appl1
18	164	95.3	100	14	US-10-357-028-6	Sequence 6, Appl1
19	164	95.3	103	14	US-10-357-028-9	Sequence 9, Appl1
20	164	95.3	117	16	US-10-467-595-27	Sequence 27, Appl1
21	164	95.3	118	10	US-09-942-024-96	Sequence 96, Appl1
22	164	95.3	118	10	US-09-942-024-96	Sequence 96, Appl1
23	164	95.3	118	15	US-10-261-161-10	Sequence 10, Appl1
24	164	95.3	347	14	US-10-100-957A-28	Sequence 28, Appl1
25	164	95.3	350	14	US-10-100-957A-30	Sequence 30, Appl1
26	164	95.3	365	10	US-09-293-670-52	Sequence 52, Appl1
27	162	94.2	35	10	US-09-962-360B-4	Sequence 4, Appl1
28	152	88.4	109	14	US-10-369-493-6364	Sequence 6364, Ap
29	149	86.6	40	10	US-09-942-024-57	Sequence 57, Appl1
30	149	86.6	40	10	US-09-942-024-58	Sequence 58, Appl1
31	149	86.6	40	10	US-09-942-024-60	Sequence 60, Appl1
32	149	86.6	40	10	US-09-942-024-61	Sequence 61, Appl1
33	149	86.6	40	10	US-09-942-024-65	Sequence 65, Appl1
34	149	86.6	40	10	US-09-942-024-65	Sequence 65, Appl1
35	149	86.6	40	10	US-09-942-024-58	Sequence 58, Appl1
36	149	86.6	40	10	US-09-942-024-60	Sequence 60, Appl1
37	149	86.6	40	10	US-09-942-024-61	Sequence 61, Appl1
38	149	86.6	40	15	US-10-261-161-82	Sequence 82, Appl1
39	149	86.6	40	15	US-10-261-161-83	Sequence 83, Appl1
40	149	86.6	40	15	US-10-261-161-85	Sequence 85, Appl1
41	149	86.6	40	15	US-10-261-161-86	Sequence 86, Appl1
42	149	86.6	40	15	US-10-261-161-90	Sequence 90, Appl1
43	149	86.6	40	15	US-10-261-161-90	Sequence 90, Appl1
44	145	84.3	104	10	US-09-942-024-20	Sequence 20, Appl1
45	145	84.3	104	10	US-09-942-024-20	Sequence 20, Appl1

# ALIGNMENTS

RESULT 1  
US-09-962-360B-9  
; Sequence 9, Application US/09962360B  
; Publication No. US20030077685A1  
; GENERAL INFORMATION:  
; /9  
; APPLICANT: Schmidt, James J.  
; APPLICANT: Stafford, Robert G.  
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi  
; TITLE OF INVENTION: Neurotoxins  
; FILE REFERENCE: 003/224/SAP  
; CURRENT APPLICATION NUMBER: US/09/962,360B  
; CURRENT FILING DATE: 2002-08-19  
; PRIOR APPLICATION NUMBER: US 60/235,050  
; PRIOR FILING DATE: 2001-09-25  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Apple Macintosh Microsoft Word 6.0  
; SEQ ID NO 9  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BONT B  
; NAME/KEY: misc\_feature  
; LOCATION: 1  
; OTHER INFORMATION: Xaa at 1 is N-fluoreceinyl-glycine  
US-09-962-360B-9  
Query Match 98.3%; Score 169; DB 10; Length 42;  
Best Local Similarity 94.3%; Pred. No. 6,6e-16;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
CY 1 LSELDRADALQXASQFEXSAKLRKYWKXNK 35  
DB 4 LSELDRADALQXASQFEXSAKLRKYWKXNK 38

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RESULT 2
US-09-942-024-4
; Sequence 4, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-942-024-4

Query Match          98.3%; Score 169; DB 10; Length 116;
Best Local Similarity 94.3%; Pred. No. 1.8e-15;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 LSELDDRADALQAXASQFEXSAKLRKRYWKNLK 35
60 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 94

RESULT 3
US-09-942-024-17
; Sequence 17, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 116
; TYPE: PR1
; ORGANISM: Mus musculus
US-09-942-024-17

Query Match          98.3%; Score 169; DB 10; Length 116;
Best Local Similarity 94.3%; Pred. No. 1.8e-15;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 LSELDDRADALQAXASQFEXSAKLRKRYWKNLK 35
60 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 94

RESULT 4
US-09-942-024-18
; Sequence 18, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
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; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 116
; TYPE: PR1
; ORGANISM: Bos taurus
US-09-942-024-18

Query Match          98.3%; Score 169; DB 10; Length 116;
Best Local Similarity 94.3%; Pred. No. 1.8e-15;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 LSELDDRADALQAXASQFEXSAKLRKRYWKNLK 35
60 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 94

RESULT 5
US-09-942-098-4
; Sequence 4, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridia1
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PR1
; ORGANISM: Homo sapiens
US-09-942-098-4

Query Match          98.3%; Score 169; DB 10; Length 116;
Best Local Similarity 94.3%; Pred. No. 1.8e-15;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 LSELDDRADALQAXASQFEXSAKLRKRYWKNLK 35
60 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 94

RESULT 6
US-09-942-098-17
; Sequence 17, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridia1
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 116
; TYPE: PR1
; ORGANISM: Mus musculus
US-09-942-098-17

Query Match          98.3%; Score 169; DB 10; Length 116;
Best Local Similarity 94.3%; Pred. No. 1.8e-15;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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QY 1 LSELDDRADALQAXASQFEXSAKLRKRYWKNLK 35  
60 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 94

Db

RESULT 7  
US-09-942-098-18  
Sequence 18, Application US/09942098  
Publication No. US20030143651A1  
GENERAL INFORMATION:  
APPLICANT: Steward, Lance B.  
APPLICANT: Fernandez-Salas, Ester  
APPLICANT: Aoki, Kei Roger  
TITLE OF INVENTION: Fret Protease Assays For Clostridial  
FILE REFERENCE: P-AR 4802  
CURRENT APPLICATION NUMBER: US/09/942,098  
CURRENT FILING DATE: 2001-08-28  
NUMBER OF SEQ ID NOS: 96  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 18  
LENGTH: 116  
TYPE: PRF  
ORGANISM: Bos taurus  
US-09-942-098-18

Query Match 98.3%; Score 169; DB 10; Length 116;  
Best Local Similarity 94.3%; Pred. No. 1.8e-15;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAXASQFEXSAKLRKRYWKNLK 35  
60 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 94

Db

RESULT 8  
US-10-357-028-10  
Sequence 10, Application US/10357028  
Publication No. US20030180931A1  
GENERAL INFORMATION:  
APPLICANT: Stuart, Susan G.  
APPLICANT: Hawkins, Phillip R.  
APPLICANT: Selthamer, Jeffrey J.  
APPLICANT: Murry, Lynn E.  
TITLE OF INVENTION: CELLUBREVIN HOMOLOGS  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/357,028  
FILING DATE: 29-Jan-2003  
PRIOR APPLICATION NUMBER: US/09/483,665  
FILING DATE: Herewith  
APPLICATION NUMBER: 08/621,018  
FILING DATE: March 22, 1996  
APPLICATION NUMBER: 08/409,373  
FILING DATE: March 23, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Hamlet-Cox, Diana  
REGISTRATION NUMBER: 33,302  
REFERENCE/DOCKET NUMBER: PF-0029-2 DIV

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-849-8886  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 116 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: GI 433075  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-10-357-028-10

Query Match 98.3%; Score 169; DB 14; Length 116;  
Best Local Similarity 94.3%; Pred. No. 1.8e-15;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAXASQFEXSAKLRKRYWKNLK 35  
60 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 94

Db

RESULT 9  
US-10-261-161-11  
Sequence 11, Application US/10261161  
Publication No. US20040072270A1  
GENERAL INFORMATION:  
APPLICANT: Steward, Lance B.  
APPLICANT: Fernandez-Salas, Ester  
APPLICANT: Aoki, Kei Roger  
TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy  
TRANSFER (FRET) Assays For Clostridial Toxins  
FILE REFERENCE: P-AR 4804  
CURRENT APPLICATION NUMBER: US/10/261,161  
CURRENT FILING DATE: 2002-09-27  
NUMBER OF SEQ ID NOS: 109  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 11  
LENGTH: 116  
TYPE: PRF  
ORGANISM: Homo sapiens  
US-10-261-161-11

Query Match 98.3%; Score 169; DB 15; Length 116;  
Best Local Similarity 94.3%; Pred. No. 1.8e-15;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAXASQFEXSAKLRKRYWKNLK 35  
60 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 94

Db

RESULT 10  
US-10-261-161-12  
Sequence 12, Application US/10261161  
Publication No. US20040072270A1  
GENERAL INFORMATION:  
APPLICANT: Steward, Lance B.  
APPLICANT: Fernandez-Salas, Ester  
APPLICANT: Aoki, Kei Roger  
TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy  
TRANSFER (FRET) Assays For Clostridial Toxins  
FILE REFERENCE: P-AR 4804  
CURRENT APPLICATION NUMBER: US/10/261,161  
CURRENT FILING DATE: 2002-09-27  
NUMBER OF SEQ ID NOS: 109  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12  
LENGTH: 116  
TYPE: PRF

ORGANISM: Mus musculus  
US-10-261-161-12

Query Match 98.3%; Score 169; DB 15; Length 116;  
Best Local Similarity 94.3%; Pred. No. 1.8e-15;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAXASQEFXSAAKLKRYKWMNKLK 35  
60 LSELDDRADALQAGASQEFXSAAKLKRYKWMNKLK 94

RESULT 11

US-10-261-161-13  
Sequence 13, Application US/10261161  
Publication No. US20040072270A1  
GENERAL INFORMATION:  
APPLICANT: Fernandez-Salas, Ester  
APPLICANT: Steward, Lance E.  
APPLICANT: Aoki, Kei-Roger  
TITLE OF INVENTION: Cell-based fluorescence resonance energy transfer (FRET) Assays for Clostridial Toxins  
FILE REFERENCE: P-AR 4804  
CURRENT APPLICATION NUMBER: US/10/261,161  
NUMBER OF SEQ ID NOS: 109  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13  
LENGTH: 116  
TYPE: PRT  
ORGANISM: Bos taurus  
US-10-261-161-13

Query Match 98.3%; Score 169; DB 15; Length 116;  
Best Local Similarity 94.3%; Pred. No. 1.8e-15;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAXASQEFXSAAKLKRYKWMNKLK 35  
60 LSELDDRADALQAGASQEFXSAAKLKRYKWMNKLK 94

RESULT 12

US-09-293-670-55  
Sequence 55, Application US/09293670  
Publication No. US20030190684A1  
GENERAL INFORMATION:  
APPLICANT: Fisher, Joseph  
APPLICANT: Lorens, James  
APPLICANT: Payan, Donald  
TITLE OF INVENTION: Multiparameter Facs Assays to Detect Alterations in  
TITLE OF INVENTION: Cellular Parameters and to Screen Small Molecule  
FILE REFERENCE: A68104/DJB/RMS/DAV  
CURRENT APPLICATION NUMBER: US/09/293,670  
CURRENT FILING DATE: 1999-04-16  
NUMBER OF SEQ ID NOS: 57  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 55  
LENGTH: 607  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-293-670-55

Query Match 98.3%; Score 169; DB 10; Length 607;  
Best Local Similarity 94.3%; Pred. No. 9.8e-15;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAXASQEFXSAAKLKRYKWMNKLK 35  
60 LSELDDRADALQAGASQEFXSAAKLKRYKWMNKLK 94

Db 61 LSELDDRADALQAGASQEFXSAAKLKRYKWMNKLK 95

RESULT 13  
US-09-962-360B-3  
Sequence 3, Application US/09962360B  
Publication No. US20030077685A1  
GENERAL INFORMATION:  
/9  
APPLICANT: Schmidt, James J.  
APPLICANT: Stafford, Robert G.  
TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi  
TITLE OF INVENTION: Neurotoxins  
FILE REFERENCE: 003/224/SAP  
CURRENT APPLICATION NUMBER: US/09/962,360B  
CURRENT FILING DATE: 2002-08-19  
PRIOR APPLICATION NUMBER: US 60/235,050  
PRIOR FILING DATE: 2001-09-25  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: Apple Macintosh Microsoft Word 6.0  
SEQ ID NO 3  
LENGTH: 35  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BONT B  
NAME/KEY: misc feature  
LOCATION: 14 and 20  
OTHER INFORMATION: Xaa at 14 is N(epsilon)-2,4-(dinitrophenyl)-lysine and Xaa at 20 ;  
OTHER INFORMATION: (fluoresceiny1)-cysteine  
US-09-962-360B-3

Query Match 97.7%; Score 168; DB 10; Length 35;  
Best Local Similarity 100.0%; Pred. No. 7.6e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAXASQEFXSAAKLKRYKWMNKLK 35  
60 LSELDDRADALQAGASQEFXSAAKLKRYKWMNKLK 95

RESULT 14

US-10-357-028-11  
Sequence 11, Application US/10357028  
Publication No. US20030180931A1  
GENERAL INFORMATION:  
APPLICANT: Stuart, Susan G.  
APPLICANT: Hawkins, Phillip R.  
APPLICANT: Sellhammer, Jeffrey J.  
APPLICANT: Murty, Lynn E.  
TITLE OF INVENTION: CELLUBREVIN HOMOLOGS  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/357,028  
FILING DATE: 29-Jan-2003  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/483,665  
FILING DATE: Hereewith  
APPLICATION NUMBER: 08/621,018  
FILING DATE: March 22, 1996



APPLICATION NUMBER: 08/409,373  
 FILING DATE: March 23, 1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Hamlet-Cox, Diana  
 REGISTRATION NUMBER: 33,302  
 REFERENCE/DOCKET NUMBER: PF-0029-2 DIV  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 650-855-0555  
 TELEFAX: 650-843-8886  
 INFORMATION FOR SEQ ID NO: 11:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 82 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 IMMEDIATE SOURCE:  
 LIBRARY: GENBANK  
 CLONE: GI 606978  
 SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
 US-10-357-028-11

Query Match 97.1%; Score 167; DB 14; Length 82;  
 Best Local Similarity 91.4%; Pred. No. 2.4e-15;  
 Matches 32; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

CY 1 LSELDDRADALQAXASQFEXSAKLRKRYWKNLK 35  
 |||||  
 Db 26 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 60

RESULT 15  
 US-09-942-024-19  
 ; Sequence 19, Application US/09942024  
 ; Publication No. US20030143650A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Steward, Lance E.  
 ; APPLICANT: Fernandez-Salas, Ester  
 ; APPLICANT: Aoki, Kei Roger  
 ; TITLE OF INVENTION: Fret Protease Assays For Botulinum  
 ; FILE REFERENCE: P-AR 4803  
 ; CURRENT APPLICATION NUMBER: US/09/942,024  
 ; CURRENT FILING DATE: 2001-08-28  
 ; NUMBER OF SEQ ID NOS: 96  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 19  
 ; LENGTH: 114  
 ; TYPE: PRT  
 ; ORGANISM: Xenopus laevis  
 ; US-09-942-024-19

Query Match 97.1%; Score 167; DB 10; Length 114;  
 Best Local Similarity 91.4%; Pred. No. 3.4e-15;  
 Matches 32; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

CY 1 LSELDDRADALQAXASQFEXSAKLRKRYWKNLK 35  
 |||||  
 Db 58 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 92

Search completed: November 1, 2004, 18:23:47  
 Job time : 70.0625 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 1, 2004, 17:52:25 ; Search time 18.125 Seconds

(without alignments)  
185.798 Million cell updates/sec

Title: US-10-802-574-3

Sequence: 1 LSELDLRADALQAXAQSFXSAKLRKRYWKNLK 35

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79: \*  
1: Dir1: \*  
2: Dir2: \*  
3: Dir3: \*  
4: Dir4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	169	98.3	116	2 B38315	synaptobrevin 2 -
2	169	98.3	116	2 JN0011	synaptobrevin 2 -
3	169	98.3	116	2 B34288	synaptobrevin 2 -
4	164	95.3	103	2 S35077	celldubrevin - rat
5	164	95.3	118	2 S52747	Vamp1 protein - hu
6	164	95.3	118	2 A38315	synaptobrevin 1 -
7	164	95.3	120	2 A32146	vesicle-associated
8	157	91.3	118	2 A34288	vesicle-associated
9	154	89.5	125	2 S40153	synaptobrevin - 1c
10	152	88.4	109	2 T33239	synaptobrevin SNB
11	115	66.9	32	2 S35555	vesicle-associated
12	115	66.9	32	2 S35555	vesicle-associated
13	115	66.9	32	2 S35555	vesicle-associated
14	112	65.1	132	2 J01522	synaptobrevin isof
15	112	65.1	152	2 J01521	synaptobrevin isof
16	108	62.8	132	2 S35553	vesicle-associated
17	106	61.6	145	2 T21318	hypothetical prote
18	87	50.6	223	2 S47654	integral membrane
19	81	47.1	115	2 S62059	synaptobrevin homo
20	75	43.6	121	2 T39073	synaptobrevin homo
21	71	41.3	117	2 S31250	synaptobrevin homo
22	68	39.5	220	2 T00801	probable synaptoch
23	64	37.2	60	2 D40088	homeotic protein H
24	64	37.2	221	2 P84741	probable synaptoch
25	63	36.6	1237	1 P84742	HIV-1 retrovirus
26	62	36.0	175	2 D61610	hypothetical prote
27	59	34.3	251	2 S64927	probable membrane
28	58	33.7	210	2 T16595	hypothetical prote
29	57.5	33.4	229	2 P86180	hypothetical prote

30	57	33.1	240	2 T47589	synaptobrevin-like
31	55	32.0	219	2 T04630	synaptobrevin homo
32	54	31.4	102	2 S44781	C30A5.4 protein -
33	54	31.4	102	2 T24909	hypothetical prote
34	54	31.4	302	2 S69725	hypothetical prote
35	53	30.8	499	2 T18791	gamma-aminobutyric
36	53	30.8	855	2 T29775	hypothetical prote
37	52.5	30.5	2326	2 T29140	hypothetical prote
38	52	30.2	183	1 TUBP84	tail fiber assembl
39	52	30.2	183	2 S13240	tail fiber assembl
40	52	30.2	788	2 T44262	transducer protein
41	52	30.2	789	2 E84236	Htr6 transducer [1
42	52	30.2	1116	2 T42213	m-tomosyn, isoform
43	51.5	29.9	1278	2 T27925	hypothetical prote
44	51	29.7	609	2 A80500	glutamine-fructose
45	51	29.7	1281	2 UC5368	dynactin 1 - mouse

#### ALIGNMENTS

##### RESULT 1

B38315

synaptobrevin 2 - human

C/Species: Homo sapiens (man)

C/Date: 14-Jun-1991 #sequence\_revision 14-Jun-1991 #text\_change 09-Jul-2004

C/Accession: B38315

R/Archer III, B.T.; Oezcelik, T.; Jahn, R.; Francke, U.; Suedhof, T.C.

U. Biol. Chem. 265, 17267-17273, 1990

A/Title: Structures and Chromosomal localizations of two human genes encoding synaptobrevin

A/Reference number: A38315; MID:91009161; PMID:1976629

A/Accession: B38315

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-116 <ARC>

A/Cross-references: UNIPROT:P19065; GB:M36205; GB:J05611; NID:G338630; PTDN:AAA60604.1; I

C/Accession: B38315

A/Accession: B38315

A/Accession: B38315

A/Accession: B38315

A/Accession: B38315

A/Accession: B38315

A/Accession: B38315

A/Accession: B38315

A/Accession: B38315

A/Accession: B38315

A/Accession: B38315

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A/Accession: B38315

A/Accession: B38315

A/Accession: B38315

A/Accession: B38315

A/Accession: B38315

A/Accession: B38315

A/Accession: B38315

A:Molecule type: mRNA  
A:Residues: 'X',48-79 <HOR>  
A:Experimental source: brain  
R:Soelner, T.; Whiteheart, S.W.; Brunner, M.; Erdjument-Bromage, H.; Geromano, S.; Tem  
Nature 362, 318-324, 1993  
A>Title: SNAP receptors implicated in vesicle targeting and fusion.  
A:Accession number: S32360; MUID:93205116; PMID:8455717  
A:Accession: S32363  
A:Molecule type: protein  
A:Residues: 31-47, 'X',49-55, 'X',57-59;67-82 <SOE>  
A:Experimental source: brain  
C:Comment: This protein is an intrinsic membrane protein of small synaptic vesicles.  
C:Superfamily: synaptobrevin  
C:Keywords: acetylated amino end; membrane trafficking; transmembrane protein  
F:2-116/Product: synaptobrevin #status predicted <MAT>  
F:95-114/Domain: transmembrane #status predicted (in mature form) #status predicted  
F:2/Modified site: acetylated amino end (Ser) (in mature form) #status predicted

Query Match 98.3%; Score 169; DB 2; Length 116;  
Best Local Similarity 94.3%; Pred. No. 3e-16;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LSELDPRADALQXASQFEXSAKLRKRYWKNLK 35  
|||||  
60 LSELDPRADALQXASQFETSAAKLRKRYWKNLK 94

## RESULT 3

B34288 synaptobrevin 2 - rat  
N:Alternate names: vesicle-associated membrane protein 2  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 01-Jun-1990 #sequence\_revision 01-Jun-1990 #text\_change 09-Jul-2004  
C:Accession: B34288; S27125  
R:Elferink, L.A.; Trimble, W.S.; Scheller, R.H.  
J. Biol. Chem. 264, 11061-11064, 1989  
A>Title: Two vesicle-associated membrane protein genes are differentially expressed in d  
A:Reference number: A34288; MUID:89291844; PMID:2472388  
A:Accession: B34288  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-116 <ELF>  
A:Cross-references: UNIPROT:Q64357; GB:M24105; GB:J04827; NID:9207626; PIDN:AAA42321.1;  
R:Schlavo, G.; Benenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta, B.R  
Nature 359, 832-835, 1992  
A>Title: Tetanus and Botulinum-B neurotoxins block neurotransmitter release by proteolyt  
A:Reference number: S27125; MUID:93063293; PMID:1331807  
A:Accession: S27125  
A:Molecule type: protein  
A:Residues: 77-99, 'X',101 <SCH>  
A:Superfamily: synaptobrevin  
C:Keywords: membrane protein; membrane trafficking; synaptic vesicle

Query Match 98.3%; Score 169; DB 2; Length 116;  
Best Local Similarity 94.3%; Pred. No. 3e-16;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LSELDPRADALQXASQFEXSAKLRKRYWKNLK 35  
|||||  
60 LSELDPRADALQXASQFETSAAKLRKRYWKNLK 94

## RESULT 4

S35077 cellubrevin - rat  
C:Species: Rattus norvegicus (Norway rat)  
C>Date: 10-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C:Accession: S35077  
R:McMahon, H.T.; Uschakov, Y.A.; Edelman, L.; Link, E.; Binz, T.; Niemann, H.; Jahn, R  
Nature 364, 346-349, 1993  
A>Title: Cellubrevin is a ubiquitous tetanus-toxin substrate homologous to a putative sy  
A:Reference number: S35077; MUID:93323976; PMID:8332193  
A:Accession: S35077

A:Molecule type: mRNA  
A:Residues: 1-103 <KCM>  
A:Cross-references: UNIPROT:Q64271; GB:S63830; NID:9388482; PIDN:AAE27554.1; PID:9388483  
C:Superfamily: synaptobrevin

Query Match 95.3%; Score 164; DB 2; Length 103;  
Best Local Similarity 91.4%; Pred. No. 1.3e-15;  
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LSELDPRADALQXASQFEXSAKLRKRYWKNLK 35  
|||||  
47 LSELDPRADALQXASQFETSAAKLRKRYWKNLK 81

## RESULT 5

S52747 Vamp1 protein - human (fragment)  
C:Species: Homo sapiens (man)  
C>Date: 19-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004  
C:Accession: S52747  
R:Gough, K.H.; Verkuylen, A.; Cosgrove, L.; Frenkel, M.J.; Ward, C.W.  
submitted to the EMBL Data Library, December 1994  
A:Description: Isolation and sequence analysis of SNAREs from human skeletal muscle.  
A:Reference number: S52747  
A:Accession: S52747  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-118 <GOU>  
A:Cross-references: UNIPROT:P23763; EMBL:248924; NID:9758107; PIDN:CAA8760.1; PID:975810  
C:Superfamily: synaptobrevin

Query Match 95.3%; Score 164; DB 2; Length 118;  
Best Local Similarity 91.4%; Pred. No. 1.5e-15;  
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LSELDPRADALQXASQFEXSAKLRKRYWKNLK 35  
|||||  
62 LSELDPRADALQXASQFESSAAKLRKRYWKNLK 96

## RESULT 6

A38315 synaptobrevin 1 - human  
C:Species: Homo sapiens (man)  
C>Date: 14-Jun-1991 #sequence\_revision 14-Jun-1991 #text\_change 09-Jul-2004  
C:Accession: A38315  
R:Archer III, B.T.; Oezcelik, T.; Jahn, R.; Francke, U.; Suedhof, T.C.  
J. Biol. Chem. 265, 17267-17273, 1990  
A>Title: Structures and chromosomal localizations of two human genes encoding synaptobrev  
A:Reference number: A38315; MUID:91009161; PMID:1976629  
A:Accession: A38315  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-118 <ARC>  
A:Cross-references: UNIPROT:P23763; GB:M36200; GB:J05611; NID:9338623; PIDN:AAA60503.1; I  
C:Genetics:  
A:Gene: GDB:SYB1; VAMP-1  
A:Cross-references: GDB:125292; OMIM:185880  
A:Map position: 12p-12p  
C:Superfamily: synaptobrevin  
C:Keywords: membrane trafficking; transmembrane protein

Query Match 95.3%; Score 164; DB 2; Length 118;  
Best Local Similarity 91.4%; Pred. No. 1.5e-15;  
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LSELDPRADALQXASQFEXSAKLRKRYWKNLK 35  
|||||  
62 LSELDPRADALQXASQFESSAAKLRKRYWKNLK 96

## RESULT 7

A32146

vesicle-associated membrane protein 1 - Pacific electric ray  
C/Species: Torpedo californica (Pacific electric ray)  
C/Date: 21-May-1990 #sequence\_revision 21-May-1990 #text\_change 09-Jul-2004  
C/Accession: A32146  
R/Trimble, W.S.; Cowan, D.M.; Scheller, R.H.  
Proc. Natl. Acad. Sci. U.S.A. 85, 4538-4542, 1988  
A/Title: VAMP-1: a synaptic vesicle-associated integral membrane protein.  
A/Reference number: A32146; MUID:88248054; PMID:3380805  
A/Accession: A32146  
A/Molecule type: mRNA  
A/Residues: 1-120 <TR>  
A/Cross-references: UNIPROT:P13701; EMBL:J03777; NID:g213245; PIDN:AAA49286.1; PID:g2132  
C/Superfamily: synaptobrevin  
C/Keywords: membrane protein

Query Match 95.3%; Score 164; DB 2; Length 120;  
Best Local Similarity 91.4%; Pred. No. 1.5e-15;  
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAXASQFEKSAKLRKRYWKXK 35  
Db 64 LSELDDRADALQAGASQFEKSAKLRKRYWKXK 98

RESULT 8  
A34288  
vesicle-associated membrane protein 1 - rat  
C/Species: Rattus norvegicus (Norway rat)  
C/Date: 01-Jun-1990 #sequence\_revision 01-Jun-1990 #text\_change 09-Jul-2004  
C/Accession: A34288  
R/Bierink, L.A.; Trimble, W.S.; Scheller, R.H.  
J. Biol. Chem. 264, 11061-11064, 1989  
A/Title: Two vesicle-associated membrane protein genes are differentially expressed in t  
A/Reference number: A34288; MUID:89291844; PMID:2472388  
A/Accession: A34288  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-118 <TR>  
A/Cross-references: UNIPROT:Q63666; GB:M24104; GB:J04827; NID:g207628; PIDN:AAA42322.1;  
C/Superfamily: synaptobrevin  
C/Keywords: membrane protein

Query Match 91.3%; Score 157; DB 2; Length 118;  
Best Local Similarity 88.6%; Pred. No. 1.4e-14;  
Matches 31; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAXASQFEKSAKLRKRYWKXK 35  
Db 62 LSELDDRADALQAGASQFEKSAKLRKRYWKXK 96

RESULT 9  
S40153  
synaptobrevin - longfin squid  
C/Species: Loligo pealeii (longfin squid)  
C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
C/Accession: S40153  
R/Bommert, K.; Kistner, A.; Hasemann, E.; Betz, H.  
submitted to the EMBL Data Library, August 1993  
A/Description: Conservation of primary structure and clostridial neurotoxin cleavage sit  
A/Reference number: S40153  
A/Accession: S40153  
A/Status: preliminary  
A/Molecule type: mRNA  
A/Residues: 1-125 <BOM>  
A/Cross-references: UNIPROT:P47194; EMBL:X74748; NID:g437855; PIDN:CAA52766.1; PID:g4378  
C/Superfamily: synaptobrevin

Query Match 89.5%; Score 154; DB 2; Length 125;  
Best Local Similarity 82.9%; Pred. No. 3.8e-14;  
Matches 29; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAXASQFEKSAKLRKRYWKXK 35

Db 69 LSELDDRADALQAGASQFEKSAKLRKRYWKXK 103

RESULT 10  
T33239  
synaptobrevin SNB-1 - Caenorhabditis elegans  
C/Species: Caenorhabditis elegans  
C/Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
C/Accession: T33239  
R/Greco, T.; Bradshaw, H.; O'Brien, D.  
submitted to the EMBL Data Library, May 1998  
A/Description: The sequence of C. elegans cosmid T10H9.  
A/Reference number: Z21306  
A/Accession: T33239  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-109 <GRE>  
A/Cross-references: UNIPROT:O02495; EMBL:AF067949; PIDN:AAC19234.1; GSPDB:GN00023; CESP:1  
A/Experimental source: strain Bristol N2; clone T10H9  
A/Genes: SNB-1; CESP:T10H9.4  
A/Map position: 5  
A/Introns: 39/3  
C/Superfamily: synaptobrevin

Query Match 88.4%; Score 152; DB 2; Length 109;  
Best Local Similarity 82.9%; Pred. No. 6.3e-14;  
Matches 29; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAXASQFEKSAKLRKRYWKXK 35  
Db 52 LSELDDRADALQAGASQFEKSAKLRKRYWKXK 86

RESULT 11  
S3555  
vesicle-associated membrane protein 2 - chicken (fragment)  
C/Species: Gallus gallus (chicken)  
C/Date: 10-Dec-1993 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004  
C/Accession: S3555  
R/Paternello, T.; Bargelloni, L.; Rossetto, O.; Schiavo, G.; Montecucco, C.  
Nature 364, 581-582, 1993  
A/Title: Neurotransmission and secretion.  
A/Reference number: S3555; MUID:93354436; PMID:8350916  
A/Accession: S3555  
A/Molecule type: DNA  
A/Residues: 1-32 <PAT>  
A/Cross-references: UNIPROT:Q7LZ64  
C/Superfamily: synaptobrevin  
C/Keywords: membrane trafficking; transmembrane protein

Query Match 66.9%; Score 115; DB 2; Length 32;  
Best Local Similarity 92.6%; Pred. No. 2.4e-09;  
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAXASQFEKSAKLR 27  
Db 6 LSELDDRADALQAGASQFEKSAKLR 32

RESULT 12  
S35554  
vesicle-associated membrane protein 2 - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 10-Dec-1993 #sequence\_revision 27-Feb-1997 #text\_change 09-Jul-2004  
C/Accession: S35554  
R/Paternello, T.; Bargelloni, L.; Rossetto, O.; Schiavo, G.; Montecucco, C.  
Nature 364, 581-582, 1993  
A/Title: Neurotransmission and secretion.  
A/Reference number: S3555; MUID:93354436; PMID:8350916  
A/Accession: S35554  
A/Status: preliminary

A:Molecule type: DNA  
 A:Residues: 1-32 <PAT>  
 A:Cross-references: UNIPROT:O35619  
 C:Superfamily: synaptobrevin

Query Match 66.9%; Score 115; DB 2; Length 32;  
 Best Local Similarity 92.6%; Pred. No. 2.4e-09;  
 Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAXASQEFKSAKLKR 27  
 |||||  
 DB 6 LSELDDRADALQAGASQEFKSAKLKR 32

## RESULT 13

S3552  
 Vesicle-associated membrane protein 1 - mouse (fragment)  
 C:Species: Mus musculus (house mouse)  
 C:Date: 10-Dec-1993 #sequence\_revision 27-Feb-1997 #text\_change 09-Jul-2004  
 C:Accession: S3552  
 R:Pattnello, T.; Bargelloni, L.; Rossetto, O.; Schiavo, G.; Montecucco, C.  
 Nature 364, 581-582, 1993  
 A:Title: Neurotransmission and secretion.  
 A:Reference number: S3552; MUID:9354436; PMID:8350916  
 A:Accession: S3552  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-32 <PAT>  
 A:Cross-references: UNIPROT:Q9CXX2  
 C:Superfamily: synaptobrevin

Query Match 66.9%; Score 115; DB 2; Length 32;  
 Best Local Similarity 92.6%; Pred. No. 2.4e-09;  
 Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAXASQEFKSAKLKR 27  
 |||||  
 DB 6 LSELDDRADALQAGASQEFKSAKLKR 32

## RESULT 14

JC1522  
 synaptobrevin isoform B - fruit fly (Drosophila melanogaster)  
 N:Alternate names: vesicle-associated membrane protein B  
 C:Species: Drosophila melanogaster  
 C:Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 09-Jul-2004  
 C:Accession: JC1522  
 R:Chin, A.C.; Burgess, R.W.; Wong, B.R.; Schwarz, T.L.; Scheller, R.H.  
 Gene 131, 175-181, 1993  
 A:Title: Differential expression of transcripts from syb, a Drosophila melanogaster gene  
 A:Reference number: JC1521; MUID:94010306; PMID:8406010  
 A:Accession: JC1522  
 A:Molecule type: DNA  
 A:Residues: 1-132 <CHI>  
 A:Cross-references: UNIPROT:P18489; GB:LI4270; NID:9290281; PIDN:AAA28924.1; PID:9290282  
 A:Note: the authors translated the codon AAG for residue 101 as Asn and CGC for residue  
 C:Comment: Gene syb comprises five exons. Splicing exons 1.2.3.4.5 results in synaptobrevin  
 C:Genetics:  
 A:Gene: syb  
 A:Cross-references: FlyBase:FBgn0003660  
 A:Introns: 16/2; 128/1  
 C:Superfamily: synaptobrevin  
 C:Keywords: membrane protein; synaptic vesicle

Query Match 65.1%; Score 112; DB 2; Length 132;  
 Best Local Similarity 62.9%; Pred. No. 2.6e-08;  
 Matches 22; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAXASQEFKSAKLKRXYWKNLK 35  
 |||||  
 DB 76 LSELGERADQLLEGASQSEQAGKLRKQWNNMK 110

## RESULT 15

JC1521  
 synaptobrevin isoform A - fruit fly (Drosophila melanogaster)  
 N:Alternate names: vesicle-associated membrane protein A  
 C:Species: Drosophila melanogaster  
 C:Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 09-Jul-2004  
 C:Accession: JC1521; UN0012  
 R:Chin, A.C.; Burgess, R.W.; Wong, B.R.; Schwarz, T.L.; Scheller, R.H.  
 Gene 131, 175-181, 1993  
 A:Title: Differential expression of transcripts from syb, a Drosophila melanogaster gene  
 A:Reference number: JC1521; MUID:94010306; PMID:8406010  
 A:Accession: JC1521  
 A:Molecule type: DNA  
 A:Residues: 1-152 <CHI>  
 A:Cross-references: UNIPROT:P18489; GB:LI4270; NID:9290281; PIDN:AAA28924.1; PID:9290283  
 A:Note: the authors translated the codon AAG for residue 101 as Asn and CGC for residue  
 R:Stedhof, T.C.; Baumeister, M.; Perin, M.S.; Jahn, R.  
 Neuron 2, 1475-1481, 1989  
 A:Title: A synaptic vesicle membrane protein is conserved from mammals to Drosophila.  
 A:Reference number: A93413; MUID:90180466; PMID:2560644  
 A:Accession: UN0012  
 A:Molecule type: mRNA  
 A:Residues: 1-92, 'F', 94-152 <SUB>  
 C:Comment: Gene syb comprises five exons. Splicing exons 1.2.3.4.5 results in synaptobrevin  
 C:Genetics:  
 A:Gene: syb  
 A:Cross-references: FlyBase:FBgn0003660  
 A:Introns: 16/2; 128/1  
 C:Superfamily: synaptobrevin  
 C:Keywords: synaptic vesicle; transmembrane protein  
 F:11-130/Domain: transmembrane #status predicted <TM>

Query Match 65.1%; Score 112; DB 2; Length 152;  
 Best Local Similarity 62.9%; Pred. No. 3e-08;  
 Matches 22; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAXASQEFKSAKLKRXYWKNLK 35  
 |||||  
 DB 76 LSELGERADQLLEGASQSEQAGKLRKQWNNMK 110

Search completed: November 1, 2004, 17:53:51  
 Job time : 19.125 secs

GenCore version 5.1.6  
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## OM protein - protein search, using sw model

Run on: November 1, 2004, 17:52:26 ; Search time 97.1875 Seconds  
(without alignments)  
207.209 Million cell updates/sec

Title: US-10-802-574-3  
Perfect score: 172  
Sequence: 1 LSELDLRADALQAXASQFEXSAKLRKRYWKNLK 35

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : Uniprot 02:.\*  
1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	169	98.3	81	2	Q8H2X7
2	169	98.3	114	2	Q6P835
3	169	98.3	114	2	AAH61396
4	169	98.3	115	1	VAM2_HUMAN
5	169	98.3	115	1	VAM2_MOUSE
6	169	98.3	116	2	Q9BUC2
7	169	98.3	116	2	Q9N0Y0
8	169	98.3	116	2	Q35619
9	169	98.3	116	2	AAH02737
10	169	98.3	116	2	AAH51105
11	169	98.3	116	2	BAC41125
12	169	98.3	135	2	Q9WUW2
13	169	98.3	142	2	Q8CHR4
14	167	97.1	113	1	VAM2_XENTIA
15	167	97.1	113	1	AAH60344
16	164	95.3	99	1	VAM3_HUMAN
17	164	95.3	103	1	VAM3_MOUSE
18	164	95.3	103	1	AAH42468
19	164	95.3	103	2	AAH60045
20	164	95.3	103	2	BAC34586
21	164	95.3	103	2	BAC34723
22	164	95.3	117	2	Q8IVC9
23	164	95.3	117	2	Q6PFR3
24	164	95.3	117	2	AAH57587
25	164	95.3	118	1	VAM1_HUMAN
26	164	95.3	118	1	VAM1_MOUSE
27	164	95.3	120	1	SYB_TORCA
28	164	95.3	182	2	Q9CXX2
29	163	94.8	114	2	Q57345
30	163	94.8	102	2	Q61QK3
31	162	94.2	102	2	Q61QK3

32	162	94.2	102	2	AAH71402	AAH71402 brachydan
33	162	94.2	119	2	Q6P835	Q6P835 brachydanio
34	162	94.2	119	2	AAH59687	AAH59687 brachydan
35	160	93.0	100	2	Q9BRV4	Q9BRV4 homo sapien
36	159	92.4	110	2	Q7S2Z5	Q7S2Z5 brachydanio
37	159	92.4	110	2	AAH59626	AAH59626 brachydan
38	159	92.4	112	2	Q57432	Q57432 fugu rubrip
39	157	92.4	116	2	Q8CH14	Q8CH14 ratius norv
40	157	91.3	117	2	Q09025	Q09025 ratius norv
41	157	91.3	118	1	VAM1_RAT	Q63666 ratius norv
42	155	90.1	86	2	Q6DLT0	Q6DLT0 lateo:abrax
43	155	90.1	110	2	Q8T897	Q8T897 halocynthia
44	155	90.1	160	2	Q86FE0	Q86FE0 schistosoma
45	154	89.5	118	2	Q6DGI1	Q6DGI1 brachydanio

## ALIGNMENTS

RESULT 1		PRELIMINARY:		PRT:		81 AA.	
ID	Q8H2X7						
AC	Q8H2X7						
DT	01-MAR-2003 (TREMBLrel. 23, Created)						
DT	01-MAR-2003 (TREMBLrel. 23, Last sequence update)						
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)						
DE	Synapto-brevin-2 (Fragment)						
OS	Oryctolagus cuniculus (Rabbit)						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.						
OX	NCBI_Taxid=9986;						
BN	[1]						
RP	SEQUENCE FROM N.A.						
RC	TISSUE=Renal collecting duct;						
RX	Pubmed=12186952;						
RA	Goutraud S., Laera A., Calamita G., Carmosino M., Prociro G.,						
RA	Rossetto O., Manucci R., Rosenthal W., Svelto M., Valenti G.;						
RT	"Functional involvement of VAMP/synapto-brevin-2 in cAMP-stimulated						
RT	aquaporin 2 translocation in renal collecting duct cells.";						
RT	J. Cell Sci. 115:3667-3674(2002).						
RL	EMBL: AF262953; AAN14408.1; ..						
DR	InterPro: IPR001388; Synapto-brevin.						
DR	Pfam: PF00957; Synapto-brevin; 1.						
DR	PRINTS: PR00219; SYNAPTOBREVIN.						
DR	ProDom: PD001229; Synapto-brevin; 1.						
DR	PROSITE: PS00412; SYNAPTOBREVIN; 1.						
FT	PROSITE: PS00892; V_SNARE; 1.						
FT	NON_TER 1 1						
FT	NON_TER 81 81						
FT	SEQUENCE 81 AA; 9357 MW; 6F171CA14775860C CRC64;						
Query Match 98.3%; Score 169; DB 2; Length 81;							
Best Local Similarity 94.3%; Pred. No. 5.1e-16;							
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;							
QY	1 LSELDLRADALQAXASQFEXSAKLRKRYWKNLK 35						
DB	32 LSELDLRADALQAXASQFEXSAKLRKRYWKNLK 66						
RESULT 2							
ID	Q6P835	PRELIMINARY;		PRT;		114 AA.	
AC	Q6P835						
DT	05-JUL-2004 (TREMBLrel. 27, Created)						
DT	05-JUL-2004 (TREMBLrel. 27, Last sequence update)						
DT	05-JUL-2004 (TREMBLrel. 27, Last annotation update)						
DE	Hypothetical protein MGCT5977.						
GN	Name=MGCT5977;						
OS	Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).						
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;						
OC	Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;						
OC	Xenopodinae; Xenopus.						





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RL Neuron 2:1475-1481(1989).
RN
RP SEQUENCE OF 31-59 AND 67-82, AND ACETYLATION.
RC SPECIES=Bovine.
RX MEDLINE=93205116; PubMed=8455717;
RA Soellner T., Whiteheart S.W., Brunner M., Erdjument-Bromage H.,
RA Geromanos S., Tempst P., Rothman J.E.;
RT "SNAP receptors implicated in vesicle targeting and fusion.";
RT Nature 362:318-324(1993).
RN
RP TISSUE SPECIFICITY.
RC SPECIES=Human.
RX MEDLINE=96332494; PubMed=8760387;
RA Jagadeesh M.N., Fernandez C.S., Hewish D.R., Macaulay S.L., Gough K.H.,
RA Grusovin J., Verkuylen A., Cosgrove L., Alafaci A., Frenkel M.J.,
RA Ward C.W.;
RT "Insulin-responsive tissues contain the core complex protein SNAP-25
RT (synaptosomal-associated protein 25) A and B isoforms in addition to
RT syntaxin 4 and synaptobrevins 1 and 2.";
RT Biochem. J. 317:945-954(1996).
RN
RP TOPOLOGY.
RC SPECIES=Human.
RX MEDLINE=95137000; PubMed=7835332;
RA Kuray U., Ahnert-Hilger G., Hartmann E., Wiedenmann B., Rapoport T.A.;
RT "Transport route for synaptobrevin via a novel pathway of insertion
RT into the endoplasmic reticulum membrane.";
RT EMBO J. 14:217-223(1995).
RN
RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 33-68 IN COMPLEX WITH BOTB.
RC SPECIES=Human.
RX MEDLINE=20392548; PubMed=10932255; DOI=10.1038/77997;
RA Hanson M.A., Stevens R.C.;
RT "Cocystal structure of synaptobrevin-II bound to botulinum neurotoxin
RT type B at 2.0 A resolution.";
RT Nat. Struct. Biol. 7:687-692(2000).
RN
RP -1- FUNCTION: Involved in the targeting and/or fusion of transport
RN vesicles to their target membrane.
RC
CC -1- SUBUNIT: Interacts with VAMP and VAMPB.
CC -1- SUBCELLULAR LOCATION: Type IV membrane protein. Neuronal synaptic
CC vesicles.
CC -1- TISSUE SPECIFICITY: Nervous system and skeletal muscle.
CC -1- SIMILARITY: Belongs to the synaptobrevin family.
CC -1- SIMILARITY: Contains 1 v-SNARE coiled-coil homology domain.
CC
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CC
DR EMBL; M36205; AAA60604.1; JOINED.
DR EMBL; M36201; AAA60604.1; JOINED.
DR EMBL; M36202; AAA60604.1; JOINED.
DR EMBL; M36203; AAA60604.1; JOINED.
DR EMBL; M36204; AAA60604.1; JOINED.
DR EMBL; A1235044; CAA12385.1; -.
DR EMBL; AF135372; AAF15551.1; -.
DR EMBL; X76199; CAA53792.1; -.
DR PIR; B38315; B38315.
DR PIR; JN0011; JN0011.
DR GeneW; HGNC:12643; VAMP2.
DR PDB; 1F83; X-ray; B=52-75, C=76-87.
DR MIM; 185881; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR InterPro; IPR001388; Synaptobrevin.
DR Pfam; PF00957; Synaptobrevin.
DR PRINTS; PR00219; SYNAPTOBREVN.
DR ProDom; PD001229; Synaptobrevin; 1.
DR PROSITE; PS00417; SYNAPTOBREVN; 1.
DR PROSITE; PS50892; V_SNARE; 1.
RC SPECIES=Rat.

KW 3D-structure; Acetylation; Coiled coil; Direct protein sequencing;
KW Multigene family; Synapse; Synaptosome; Transmembrane.
FT INIT MET 0
FT DOMAIN 1 93 Cytoplasmic (potential).
FT TRANSMEM 94 113 Anchor for type IV membrane protein
FT 114 115 (potential).
FT DOMAIN 114 115 Vesicular (potential).
FT MOD_RES 1 1 N-acetylsertine.
FT DOMAIN 30 90 v-SNARE coiled-coil homology.
SQ SEQUENCE 115 AA; 12517 MW; 388B79FD021AD81E CSc64;

Query Match 98.3%; Score 169; DB 1; Length 115;
Best Local Similarity 94.3%; Pred. No. 7,3e-16;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 ISELDPRADALQAXASQFEXSAKIKRYWKNTK 35
Db 59 ISELDPRADALQAGASQFETSMAKIKRYWKNTK 93

RESULT 5
VAMP2_MOUSE STANDARD; PRT; 115 AA.
ID VAMP2_MOUSE
AC Q64357;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Vesicle-associated membrane protein 2 (VAMP-2) (Synaptobrevin 2).
GN Name=Vamp2; Synonyms=Synd2;
OS Mus musculus (Mouse); and
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
NCBI_Taxid=10090, 10116;
RN
RX SEQUENCE FROM N.A.
RC SPECIES=Rat;
RX MEDLINE=89291844; PubMed=2472368;
RA Eiferink L.A., Trimble W.S., Scheller R.H.;
RT "Two vesicle-associated membrane protein genes are differentially
RT expressed in the rat central nervous system.";
RT J. Biol. Chem. 264:11061-11064(1989).
RN
RN [2]
RN SEQUENCE FROM N.A.
RC SPECIES=Mouse;
RX MEDLINE=98104125; PubMed=9430681;
RA Martin L.B., Shewan A., Millar C.A., Gould G.W., James D.E.;
RT "Vesicle-associated membrane protein 2 plays a specific role in the
RT insulin-dependent trafficking of the facilitative glucose transporter
RT GLUT4 in 3T3-L1 adipocytes.";
RT J. Biol. Chem. 273:1444-1452(1998).
RN
RN [3]
RN X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 1-96 IN COMPLEX WITH STX1A
RN AND SNAP25.
RC SPECIES=Rat;
RX MEDLINE=8430524; PubMed=9759724; DOI=10.1038/26412;
RA Sutton R.B., Fasshauer D., Jahn R., Brunger A.T.;
RT "Crystal structure of a SNARE complex involved in synaptic exocytosis
RT at 2.4 A resolution.";
RT Nature 395:347-353(1998).
RN
RN [4]
RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 29-93 IN COMPLEX WITH STX1A;
RN CPLX1 AND SNAP25, AND NMR ANALYSIS.
RC SPECIES=Rat;
RX MEDLINE=21822661; PubMed=11832227;
RA Chen X., Tomchick D.R., Kovrigin E., Arac D., Machius M.,
RA Suedhof T.C., Rizo J.;
RT "Three-dimensional structure of the complexin/SNARE complex.";
RT Neuron 33:397-409(2002).
RN
RN [5]
RN X-RAY CRYSTALLOGRAPHY (1.45 ANGSTROMS) OF 28-89 IN COMPLEX WITH STX1A
RN AND SNAP25.
RC SPECIES=Rat;

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RX MEDLINE:22499607; PubMed:12496247; DOI=10.1074/jbc.M211889200;  
 RA Ernst U.A., Bringer A.I.,  
 RT "High resolution structure, stability, and synaptobrevin binding of a  
 RL truncated neuronal SNARE complex.";  
 CC J. Biol. Chem. 278:8630-8636 (2003).  
 CC -1- FUNCTION: Involved in the targeting and/or fusion of transport  
 CC vesicles to their target membrane.  
 CC -1- SUBUNIT: Interacts with VAMP and VAMP (By similarity). Part of the  
 CC SNARE core complex containing SNAP25, VAMP2 and STX1A. This  
 CC complex binds to CPLX1.  
 CC -1- SUBCELLULAR LOCATION: Type IV membrane protein. Neuronal synaptic  
 CC vesicles.  
 CC -1- TISSUE SPECIFICITY: Nervous system specific. A higher level  
 CC expression is seen in the brain as compared to the spinal cord.  
 CC -1- SIMILARITY: Belongs to the synaptobrevin family.  
 CC -1- SIMILARITY: Contains 1 v-SNARE coiled-coil homology domain.  
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 CC EMBL: M24105; AAA42321.1; -  
 CC EMBL: U60150; AAB03463.1; -  
 CC PIR: B34288; B34288.  
 CC PDB: 1K1L; X-ray; A=26-91.  
 CC PDB: 1N7S; X-ray; A=26-88.  
 CC PDB: 1SFC; X-ray; A/E/I=1-95.  
 CC MGD: MG1:131327; Vamp2.  
 CC RGD: 3949; Vamp2.  
 CC InterPro: IPR001388; Synaptobrevin.  
 CC Pfam: PF00957; Synaptobrevin; 1.  
 CC PRINTS: PR00219; SYNAPTOBREVN.  
 CC PRODOM: PD001229; Synaptobrevin; 1.  
 CC PROSITE: PS00417; SYNAPTOBREVN; 1.  
 CC 3D-structure: Acetylation; Coiled coil; Multigene family;  
 CC Polymorphism; Synapse; Synaptosome; Transmembrane.  
 CC INIT MET 0 By similarity.  
 CC DOMAIN 1 93 Cytoplasmic (Potential).  
 CC TRANSMEM 94 113 Anchor for type IV membrane protein  
 CC (Potential).  
 CC FT DOMAIN 114 115 Vesicular (Potential).  
 CC FT MOD\_RES 1 1 N-acetylserine (By similarity).  
 CC FT DOMAIN 30 90 V-SNARE coiled-coil homology.  
 CC FT VARIANT 110 110 I -> II.  
 CC FT VARIANT 111 111 V -> I.  
 CC FT HELIX 28 67  
 CC FT SEQUENCE 115 AA; 12559 MW; EA400D6291ABF0BC CRC64;  
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 CC Best Local Similarity 94.3%; Pred. No. 7.3e-16;  
 CC Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
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 CC QY 1 LSELDDRADALQXASQFEXSAKLRKRYWKNLX 35  
 CC DB 59 LSELDDRADALQXASQFEXSAKLRKRYWKNLX 93  
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 CC RESULT 6  
 CC Q9BUC2 PRELIMINARY; PRT; 116 AA.  
 CC AC Q9BUC2;  
 CC DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 CC DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 CC DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 CC DE Vesicle-associated membrane protein 2 (Synaptobrevin 2).  
 CC GN Name:VAMP2;  
 CC OS Homo sapiens (human).  
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 CC NCBI\_TaxID=9606;  
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 CC RN [1]  
 CC RP SEQUENCE FROM N.A.  
 CC RC TISSUE=Brain, Lung, and Testis;  
 CC RA MEDLINE:22388257; PubMed:12477932;  
 CC RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 CC RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 CC RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Bhat N.K.,  
 CC RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 CC RA Datschenko L., Marsina K., Farmer A.A., Rubin G.M., Hong L.,  
 CC RA Stopleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 CC RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Frange C.,  
 CC RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,  
 CC RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 CC RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,  
 CC RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 CC RA Raley U., Helton E., Ketterman W., Madan A., Rodrigues S., Sanchez A.,  
 CC RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 CC RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 CC RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,  
 CC RA Krzywinski M.I., Skalka U., Smalins D.E., Scherch A., Schein J.E.,  
 CC RA Jones S.J., Marra M.A.;  
 CC RT "Generation and initial analysis of more than 15,000 full-length human  
 CC and mouse cDNA sequences";  
 CC Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 CC  
 CC RL [2]  
 CC RN SEQUENCE FROM N.A.  
 CC RP TISSUE=Brain;  
 CC RC TISSUE=Brain;  
 CC RA Strausberg R.;  
 CC RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
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 CC RN [3]  
 CC RN SEQUENCE FROM N.A.  
 CC RP TISSUE=Testis;  
 CC RC Strausberg R.;  
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 CC RN [4]  
 CC RN SEQUENCE FROM N.A.  
 CC RC Strausberg R.;  
 CC RA Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
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 CC RL EMBL: BC002737; AA02737.3; -  
 CC DR EMBL: BC019608; AA119608.1; -  
 CC DR EMBL: BC033870; AA133870.1; -  
 CC DR HSP: Q9WUW2; 1SFC.  
 CC DR InterPro: IPR001388; Synaptobrevin.  
 CC DR Pfam: PF00957; Synaptobrevin; 1.  
 CC DR PRINTS: PR00219; SYNAPTOBREVN.  
 CC DR PRODOM: PD001229; Synaptobrevin; 1.  
 CC DR PROSITE: PS00417; SYNAPTOBREVN; 1.  
 CC DR PROSITE: PS00892; V-SNARE; 1.  
 CC DR SEQUENCE 116 AA; 12663 MW; 9CD679C4FF1B5A8 CRC64;  
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 CC Query Match 98.3%; Score 169; DB 2; Length 116;  
 CC Best Local Similarity 94.3%; Pred. No. 7.3e-16;  
 CC Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 CC  
 CC QY 1 LSELDDRADALQXASQFEXSAKLRKRYWKNLX 35  
 CC DB 60 LSELDDRADALQXASQFEXSAKLRKRYWKNLX 94  
 CC  
 CC RESULT 7  
 CC Q9N0Y0 PRELIMINARY; PRT; 116 AA.  
 CC AC Q9N0Y0;  
 CC DT 01-OCT-2000 (TrEMBLrel. 15, Created)  
 CC DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 CC DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 CC DE VAMP-2.  
 CC GN Macaca mulatta (Rhesus macaque).  
 CC OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

OC Cercopithecinae; Macaca.  
 OX NCBI\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Hippocampus;  
 RA Jensen M.J., Smith L.A.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
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 DR HSSP: Q9MUW2; ISFC.  
 DR InterPro: IPR001388; Synaptobrevin.  
 DR Pfam: PF00357; Synaptobrevin; 1.  
 DR PRINTS: PR00219; SYNAPTOBREVN.  
 DR Prodom: PD001229; Synaptobrevin; 1.  
 DR PROSITE: PS00417; SYNAPTOBREVN; 1.  
 DR PROSITE: PS50892; V\_SNAKE; 1.  
 SQ SEQUENCE 116 AA; 12663 MW; 9CD679C4F6F1B5A8 CRC64;

Query Match 98.3%; Score 169; DB 2; Length 116;  
 Best Local Similarity 94.3%; Pred. No. 7.3e-16;  
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDPRADALQAXAOFEXSAKLRKYWKXNLK 35  
 DB 60 LSELDPRADALQAGASOFETSAAKLRKYWKXNLK 94

RESULT 8  
 O35619 PRELIMINARY; PRT; 116 AA.  
 ID O35619;  
 AC O35619;  
 DT 01-JAN-1998 (TREMBLrel. 05, Created)  
 DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)  
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)  
 DE Vesicle associated membrane protein 2.  
 GN Name=Vamp2; Synonyms=mvVAMP-2;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Olsen S.K., Doeire S., Corley R.B.;  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF007168; AAB62931.1; -  
 DR PIR: S35554; S35554.  
 DR HSSP: Q9MUW2; ISFC.  
 DR MGD: MGI:1313277; Vamp2.  
 DR GO: GO:0030141; C:secretory granule; IDA.  
 DR GO: GO:0030672; C:synaptic vesicle membrane; IDA.  
 DR GO: GO:0042589; C:zymogen granule membrane; IDA.  
 DR GO: GO:0005516; F:calmodulin binding; IDA.  
 DR GO: GO:0005543; F:phospholipid binding; IDA.  
 DR GO: GO:0000149; F:SNARE binding; IDA.  
 DR GO: GO:0017156; P:calcium ion-dependent exocytosis; IDA.  
 DR GO: GO:0017157; P:regulation of exocytosis; IDA.  
 DR InterPro: IPR001388; Synaptobrevin.  
 DR Pfam: PF00957; Synaptobrevin; 1.  
 DR PRINTS: PR00219; SYNAPTOBREVN.  
 DR Prodom: PD001229; Synaptobrevin; 1.  
 DR PROSITE: PS00417; SYNAPTOBREVN; 1.  
 DR PROSITE: PS50892; V\_SNAKE; 1.  
 SQ SEQUENCE 116 AA; 12677 MW; 4F1DD565549D0A CRC64;

Query Match 98.3%; Score 169; DB 2; Length 116;  
 Best Local Similarity 94.3%; Pred. No. 7.3e-16;  
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDPRADALQAXAOFEXSAKLRKYWKXNLK 35  
 DB 60 LSELDPRADALQAGASOFETSAAKLRKYWKXNLK 94

RESULT 9  
 AAH02737 PRELIMINARY; PRT; 116 AA.  
 ID AAH02737;  
 AC AAH02737;  
 DT 14-APR-2004 (TREMBLrel. 27, Created)  
 DT 14-APR-2004 (TREMBLrel. 27, Last sequence update)  
 DT 14-APR-2004 (TREMBLrel. 27, Last annotation update)  
 DE Vesicle-associated membrane protein 2 (Synaptobrevin 2).  
 GN VAMP2  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,  
 RA Diatchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein W.J., Tsai T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huylk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalske U., Smalish D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC002737; AAH02737.3; -  
 SQ SEQUENCE 116 AA; 12663 MW; 9CD679C4F6F1B5A8 CRC64;

Query Match 98.3%; Score 169; DB 2; Length 116;  
 Best Local Similarity 94.3%; Pred. No. 7.3e-16;  
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDPRADALQAXAOFEXSAKLRKYWKXNLK 35  
 DB 60 LSELDPRADALQAGASOFETSAAKLRKYWKXNLK 94

RESULT 10  
 AAH55105 PRELIMINARY; PRT; 116 AA.  
 ID AAH55105;  
 AC AAH55105;  
 DT 14-APR-2004 (TREMBLrel. 27, Created)  
 DT 14-APR-2004 (TREMBLrel. 27, Last sequence update)  
 DT 14-APR-2004 (TREMBLrel. 27, Last annotation update)  
 DE Vesicle-associated membrane protein 2.  
 GN Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,  
 RA Diatchenko L., Marisina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein W.J., Tsai T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huylk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalske U., Smalish D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932;

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stempleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., Mesman P.J., McKernan K.T., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Ketteman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmitz J., Myers R.M., Buterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalios D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.,  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 [2]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Strausberg R.;  
 DR EMBL; BC055105; AAH55105.1; -  
 SQ SEQUENCE 116 AA; 12691 MW; 4A0DD056B5409D0A CRC64;  
 Query Match 98.3%; Score 169; DB 2; Length 116;  
 Best Local Similarity 94.3%; Pred. No. 7.3e-16;  
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 LSELDRADALQAXAQEFEXSAKLKRYKWWXNLK 35  
 Db 60 LSELDRADALQAGASQFETSAKLKRYKWWXNLK 94  
 RESULT 11  
 BAC41125 PRELIMINARY; PRT; 116 AA.  
 AC BAC41125;  
 DT 14-APR-2004 (TREMBLrel. 27, Created)  
 DT 14-APR-2004 (TREMBLrel. 27, Last annotation update)  
 DT 14-APR-2004 (TREMBLrel. 27, Last annotation update)  
 DE 15 days embryo brain cDNA, RIKEN full-length enriched library,  
 DE clone:G630012G02 product:unclassified, full insert sequence.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Brain;  
 RC MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 60,770 full-length cDNAs.";  
 Nature 420:563-573(2002).  
 RL Nature 420:563-573(2002).  
 RN [2]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Brain;  
 RC MEDLINE=21085660; PubMed=11217851;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 Nature 409:685-690(2001).  
 RL Nature 409:685-690(2001).  
 RN [3]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Brain;  
 RC MEDLINE=9929253; PubMed=10349636;  
 RA Carninci P., Hayashizaki Y.,  
 RT "High-efficiency full-length cDNA cloning.";  
 Meth. Enzymol. 303:19-44(1999).  
 RL [4]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Brain;

RX MEDLINE=20499374; PubMed=11042159;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.,  
 RT "Normalization and subtraction of cap-tipper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 Genome Res. 10:1617-1630(2000).  
 RL [5]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Brain;  
 RC MEDLINE=20530913; PubMed=11076861;  
 RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Kono H., Akiyama Y., Nishi K., Katsunai T., Tashiro H., Itoh M.,  
 RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwara K., Inoue K., Togawa Y., Izawa M., Ohara E., Matsubara M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsura S., Kawai U.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.,  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer.";  
 Genome Res. 10:1757-1771(2000).  
 RL [6]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Brain;  
 RA Adachi J., Aizawa K., Akimura T., Arahawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuta M., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,  
 RA Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno K., Ohnato N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sato H.,  
 RA Sasaki D., Shibata K., Shingawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeida Y., Tanaka T.,  
 RA Tomaru A., Tova T., Yasunishi A., Muramatsu M., Hayashizaki Y.,  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK090178; BAC41125.1; -  
 SQ SEQUENCE 116 AA; 12691 MW; 4A0DD056B5409D0A CRC64;  
 Query Match 98.3%; Score 169; DB 2; Length 116;  
 Best Local Similarity 94.3%; Pred. No. 7.3e-16;  
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 LSELDRADALQAXAQEFEXSAKLKRYKWWXNLK 35  
 Db 60 LSELDRADALQAGASQFETSAKLKRYKWWXNLK 94  
 RESULT 12  
 Q9RUM2 PRELIMINARY; PRT; 135 AA.  
 AC Q9RUM2;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)  
 DE Vesicle associated membrane protein 2B.  
 GN Name=vamp2;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RC MEDLINE=99297576; PubMed=10371166;  
 RX Mandic R., Lowe A.W.,  
 RT "Characterization of an alternatively spliced isoform of rat vesicle  
 RT associated membrane protein-2 (VAMP-2)."  
 FEBS Lett. 451:209-213(1999).  
 RL EMBL; AJ133104; CAB43509.1; -  
 DR InterPro; IPR001388; SynaptoBrevin.  
 DR Pfam; PF00957; SynaptoBrevin.1.  
 DR PRINTS; PR00219; SynaptoBrevin.  
 DR ProDom; PD001229; SynaptoBrevin.1.



Query Match 97.1%; Score 167; DB 1; Length 113;  
 Best Local Similarity 91.4%; Pred. No. 1.4e-15;  
 Matches 32; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDPRADALQAXASQFEXSAKXLRKXWKNLK 35  
 |||||  
 DB 57 LSELDPRADALQAGASQFETSAKXLRKXWKNMK 91  
 |||||

## RESULT 15

AAH60344 PRELIMINARY; PRT; 114 AA.

ID AAH60344

AC AAH60344;

DT 02-MAR-2004 (TRENBLrel. 27, Created)

DT 02-MAR-2004 (TRENBLrel. 27, Last sequence update)

DT 02-MAR-2004 (TRENBLrel. 27, Last annotation update)

DE VAMP2-B-prov protein.

GN VAMP2-B-PROV.

OS Xenopus laevis (African clawed frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;

OC Xenopodinae; Xenopus; Xenopus.

OC NCBI\_TaxID=8355;

OX

RN (1)

RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;

RX MEDLINE=22341132; PubMed=12454917;

RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,

RA Richardson P.;

RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus

RT Initiative.";

RL Dev. Dyn. 225:384-391 (2002).

RN (2)

RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;

RX MEDLINE=22388257; PubMed=12477932;

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Sherman C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein W.J., Ustin T.B., Toshblyuk S., Carinci P., Prange C.,

RA Raha S.S., Loguélano N.A., Peters G.J., Abramson R.D., Mullany S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.O., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Kerteman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,

RA Krzywinski M.I., Skalska U., Smalins D.E., Scherch A., Schein J.E.,

RA Jones S.J., Mair M.A.;

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences.";

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RN (3)

RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;

RA Klein S., Strausberg R.;

RA Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.

RA EMBL; BC060344; AAH60344.1; -

SO SEQUENCE 114 AA; 12472 MW; AEF2EDDCDF2DIDBF CRC64;

Query Match 97.1%; Score 167; DB 2; Length 114;  
 Best Local Similarity 91.4%; Pred. No. 1.4e-15;

Matches 32; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDPRADALQAXASQFEXSAKXLRKXWKNLK 35  
 |||||  
 DB 58 LSELDPRADALQAGASQFETSAKXLRKXWKNMK 92  
 |||||

Search completed: November 1, 2004, 17:59:09  
 Job time : 99.1875 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2004, 17:52:26 / Search time 90 Seconds  
(without alignments)  
139,506 Million cell updates/sec

Title: US-10-802-574-4

Perfect score: 173  
Sequence: 1 ISELDPRADALQAGSXFEKSAKUKRKYWNILX 35

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	170	98.3	37	2	AAR86822 VAMP isoform-1
2	170	98.3	40	4	AAB50301 VAMP2 pep
3	170	98.3	40	4	AAB48582 VAMP2 pep
4	170	98.3	42	5	AAO15163 Clostridi
5	170	98.3	54	3	AAB39482 Gene 49 h
6	170	98.3	62	2	AAR86821 VAMP isoform-1
7	170	98.3	115	7	ADE57598 Human Pro
8	170	98.3	115	7	ADE57612 Rat Prote
9	170	98.3	115	7	ADE60831 Human Pro
10	170	98.3	115	7	ADE57606 Human Pro
11	170	98.3	115	7	ADE60829 Rat Prote
12	170	98.3	115	7	ADE57600 Rat Prote
13	170	98.3	115	7	ADE57604 Rat Prote
14	170	98.3	115	7	ADE57596 Rat Prote
15	170	98.3	115	7	ADE57602 Human Pro
16	170	98.3	115	7	ADE57610 Human Pro
17	170	98.3	115	7	ADE57592 Rat Prote
18	170	98.3	115	7	ADE57594 Human Pro
19	170	98.3	115	7	ADE57614 Human Pro
20	170	98.3	115	7	ADE57608 Rat Prote
21	170	98.3	116	2	AAW30104 Vesicle-a
22	170	98.3	116	2	AAW43425 Rat Vesic
23	170	98.3	116	3	AAW88243 Bovine sy
24	170	98.3	116	5	ABP43681 VAMP-2 se
25	170	98.3	116	6	ABP76220 Human GEN

26	170	98.3	116	6	AAE36664
27	170	98.3	116	7	ABW01719
28	170	98.3	116	7	ABW01718
29	170	98.3	116	7	ABW01705
30	170	98.3	116	7	ADG89011
31	170	98.3	116	8	ADM97006
32	170	98.3	116	8	ADM97007
33	170	98.3	116	8	ADM97005
34	170	98.3	368	3	AAV43843
35	170	98.3	368	7	ADP90403
36	170	98.3	608	3	AAV43845
37	170	98.3	609	7	ADP90406
38	169	97.7	35	5	AAO15158
39	168	97.1	82	3	ADG89012
40	168	97.1	82	7	ABW01720
41	168	97.1	114	8	ADM97008
42	168	97.1	114	8	ADM97008
43	165	95.4	35	2	AAR86824
44	165	95.4	100	2	AAW04182
45	165	95.4	100	3	AAV88240

## ALIGNMENTS

RESULT 1  
ID AAR86822 standard; peptide: 37 AA.

AC AAR86822;  
DT 15-AUG-1996 (first entry)

DE VAMP isoform-1 residues 60-94 (plus N- and C-terminal cysteines).

KW VAMP; vesicle-associated membrane protein; SNAP-25; syntaxin;  
neurotransmitter; neurotoxin; botulinum; botulinism; cleavage; substrate;  
antibody; detection; assay.

OS Synthetic.

PH Key Location/Qualifiers

FT Misc-difference 1 /label= N-terminal Cysteine

FT Peptide /note= "may be present to attach peptide to solid-phase"

FT Misc-difference 37 /label= C-terminal cysteine

FT /note= "may be present to attach to peptide to solid-phase"

MO9533850-A1.

14-DEC-1995.

02-JUN-1995; 95WO-GB001279.

03-JUN-1994; 94GB-00011138.

(MICR-) MICROBIOLOGICAL RES AUTHORITY.

(CAMR-) CAMR CENT APPLIED MICROBIOLOGY & RES.

Shone CC, Hallis B, James BAF, Quinn CP,

WPI, 1996-040249/04.

Assay for botulinum or tetanus toxin - by combining test cpd. with substrate which is cleaved by the toxin, and antibody specific for the cleaved but not uncleaved substrate.

Example 1; Page 28-29; 48pp; English.

CC The botulinum neurotoxins possess highly specific zinc-endopeptidase  
 CC activities within their light sub-units. Depending on the neurotoxin type  
 CC these act to cleave small proteins within the nerve cell which are  
 CC involved in neurotransmitter release. Antibodies are used in assays which  
 CC detect cleaved but not uncleaved substrate. An assay for botulinum type B  
 CC uses the present sequence as a substrate. It is VAMP (vesicle-associated  
 CC membrane protein) isoform-1, residues 60-94. The VAMP peptide can be  
 CC attached by a C- or N-terminal cysteine to a solid phase  
 XX  
 SQ Sequence 37 AA;

Query Match 98.3%; Score 170; DB 2; Length 37;  
 Best Local Similarity 94.3%; Pred. No. 4,8e-18;  
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXPEFSAAKLKRYKWMNKLK 35  
 |||||  
 2 LSELDDRADALQAGASQFETSAAKLKRYKWMNKLK 36

RESULT 2  
 AAB50301  
 ID AAB50301 standard; peptide; 40 AA.

AC AAB50301;

DT 08-MAR-2001 (first entry)

XX VAMP2 peptide.

KM VAMP2; antibacterial; Botulinum toxin inhibitor; BttxB; previn;  
 KM tetanus neurotoxin; buforin.

XX Unidentified.

XX MO200069891-A2.

XX 23-NOV-2000.

XX 15-MAY-2000; 2000WC-US013215.

XX 17-MAY-1999; 99US-0134446P.

XX (USSA ) US DEPT OF THE ARMY.

XX Gordon RK, Moorad DR, Doctor BP, Garcia GE;

XX WPI; 2001-025001/03.

XX Novel Previn compounds useful for inhibiting the protease activity of  
 PT Botulinum B and tetanus toxins.

XX Disclosure; Page 5; 47pp; English.

XX The present sequence was investigated in the search for Botulinum toxin  
 CC inhibitors (BttxB). Previn compounds which inhibit the enzymatic activity  
 CC of BttxB and tetanus neurotoxins were isolated. Previn may be used to  
 CC construct compounds such as buforinins

XX Sequence 40 AA;

Query Match 98.3%; Score 170; DB 4; Length 40;  
 Best Local Similarity 94.3%; Pred. No. 5,2e-18;  
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXPEFSAAKLKRYKWMNKLK 35  
 |||||  
 6 LSELDDRADALQAGASQFETSAAKLKRYKWMNKLK 40

RESULT 3  
 AAB48582  
 ID AAB48582 standard; peptide; 40 AA.

XX  
 AC AAB48582;  
 XX 08-MAR-2001 (first entry)  
 DT  
 XX VAMP2 peptide.  
 DE  
 XX Buforin; Botulinum toxin B; BttxB; Tetanus neurotoxin; endoprotease;  
 KM antibacterial; VAMP2; synapcobrevin.  
 KM  
 XX

XX Unidentified.  
 XX WO200069895-A2.  
 XX 23-NOV-2000.

XX 11-MAY-2000; 2000WC-US012909.

XX 14-MAY-1999; 99US-0134216P.

XX (USSA ) US DEPT OF THE ARMY.

XX Garcia GE, Gordon RK, Moorad DR, Doctor BP;

XX WPI; 2001-102250/11.

XX Novel peptides capable of inhibiting the enzymatic activity of Botulinum  
 PT toxin B, and Tetanus neurotoxins useful for preventing or treating toxic  
 PT poisoning such as Botulinum toxin and tetanus poisoning.

XX Disclosure; Page 5; 47pp; English.

XX The present sequence is one of a number of peptide or peptide-like  
 CC compounds, designated buforins, which inhibit the enzymatic activity of  
 CC Botulinum toxin B (BttxB) and tetanus neurotoxins. The buforins are  
 CC useful for treating Botulinum or tetanus intoxication by administering a  
 CC composition comprising a buforin to the subject prior to the contact with  
 CC BttxB or tetanus intoxication. Antibodies specific for buforins are  
 CC useful for detecting buforins by forming immunocomplexes. The buforins  
 CC have improved circulatory half-life, solubility, resistance to  
 CC degradation and interaction with the active site of the toxin

XX Sequence 40 AA;

Query Match 98.3%; Score 170; DB 4; Length 40;  
 Best Local Similarity 94.3%; Pred. No. 5,2e-18;  
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXPEFSAAKLKRYKWMNKLK 35  
 |||||  
 6 LSELDDRADALQAGASQFETSAAKLKRYKWMNKLK 40

RESULT 4  
 AAO15163  
 ID AAO15163 standard; peptide; 42 AA.

XX AAO15163;

XX 02-SEP-2002 (first entry)

XX Clostridial neurotoxin protease substrate peptide 2.

XX Clostridial neurotoxin substrate; botulinum neurotoxin substrate; FRET;

XX fluorescence resonant energy transfer assay; quenched-signal;

XX Clostridial neurotoxin detection; food.

XX Unidentified.

XX Key Location/Qualifiers  
 FH Modified-site 1  
 FT /note= "N-fluoresceinyl-glycine"  
 FT Cleavage-site 20..21



/note="The peptide is cleaved between these two residues  
by the clostridial neurotoxin"

FT FT /note="The peptide is cleaved between these two residues  
FT FT by the clostridial neurotoxin"  
XX XX  
XX MO200225284-A2.  
XX  
XX 28-MAR-2002.  
XX  
XX 25-SEP-2001; 2001WO-US030188.  
XX  
XX 25-SEP-2000; 2000US-0235050P.  
XX  
XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.  
XX  
XX Schmidt JJ, Stafford RG;  
XX WPI; 2002-499829/53.  
XX  
XX Substrate useful in e.g. an assay for the protease activity of  
PT clostridial neurotoxin, comprises modified peptide or protein.  
XX  
XX Claim 24; Page 15; 48pp; English.  
XX  
XX The invention comprises clostridial neurotoxin substrate peptides which  
CC can serve as fluorescence resonant energy transfer assay (FRET) or  
CC quenched-signal substrates in assays for the proteolytic activities of  
CC clostridial neurotoxins. The invention further comprises clostridium  
CC botulinum neurotoxin substrate peptides that can serve as immobilised  
CC substrates (i.e. bound to a solid phase) in assays for the proteolytic  
CC activities of clostridial neurotoxins. The clostridial (including the  
CC clostridium botulinum) neurotoxin substrate peptides are useful for  
CC detecting the presence of clostridial neurotoxins in a sample (e.g. food  
CC or an environmental sample). The present amino acid sequence represents a  
CC clostridial neurotoxin substrate peptide of the invention  
XX  
XX Sequence 42 AA;  
SQ  
Query Match 98.3%; Score 170; DB 5; Length 42;  
Best Local Similarity 94.3%; Pred. No. 5,5e-18;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 LSELDDRADALQAGASXFEKSAKLRKRYWKNLK 35  
Db 4 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 38  
RESULT 5  
AAB39482  
ID AAB39482 standard; protein; 54 AA.  
XX  
XX AAB39482;  
XX  
XX 02-FEB-2001 (first entry)  
XX  
XX Gene 49 human secreted protein homologous amino acid sequence #14.  
XX  
XX Human; secreted protein; diagnosis; cytostatic; immunosuppressive;  
KW neotropic; neuroprotective; antiviral; antiallergic; hepatotropic;  
KW antidiabetic; antiinflammatory; antitumor; vulnary; anticonvulsant;  
KW antibacterial; antifungal; antiparasitic; cardiac; gene therapy;  
KW food additive; preservative; chromosome identification; cancer;  
KW female reproductive system disorder; immune disorder; wound healing;  
KW cardiovascular disorder; neurological disease; infectious disease;  
KW infection.  
XX  
XX Bos taurus.  
XX  
XX WO200058340-A2.  
XX  
XX 05-OCT-2000.  
XX  
XX 23-MAR-2000; 2000WO-US007724.  
XX  
XX 26-MAR-1999; 99US-0126510P.  
PR

PR 07-JUN-2000; 2000US-0174850P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Ruben SM, Komatsoulis G;  
XX WPI; 2000-594638/56.  
XX  
XX Fifty nucleic acid molecules encoding human secreted proteins, useful in  
PT the prevention, treatment and diagnosis of cancer, immune disorders,  
PT cardiovascular disorders and neurological diseases.  
XX  
XX Disclosure; Page 390; 391pp; English.  
XX  
XX The polynucleotide sequences given in AAC74337 to AAC74386 encode the  
CC human secreted proteins given in AAB39402 to AAB39451. AAB39452 to  
CC AAB39484 represent human secreted polypeptide sequences and proteins  
CC homologous to them, which are given in the exemplification of the present  
CC invention. Human secreted proteins have activities based on the tissues  
CC and cells the genes are expressed in. Example of activities include:  
CC cytostatic; immunosuppressive; neotropic; neuroprotective; antiviral;  
CC antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;  
CC vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic; and  
CC cardiac. The polynucleotides and polypeptides are useful for preventing,  
CC treating or ameliorating a medical condition in e.g. humans, mice,  
CC rabbits, goats, horses, cats, dogs, chickens or sheep. The polypeptides  
CC can also be used as a food additive or preservative to increase or  
CC decrease storage capabilities. The polynucleotide are useful for  
CC chromosome identification. They are also useful as probes for diagnosing  
CC a disorder related to the female reproductive system, particularly breast  
CC and/or ovarian cancer. They are also useful in the gene therapy of breast  
CC cancer and ovarian cancer. Secreted protein nucleic acids, proteins, antibodies,  
CC agonists and antagonists are useful in the diagnosis, treatment and  
CC prevention of: (a) cancer; (b) immune disorders; (c) cardiovascular  
CC disorders; (d) wound healing; (e) neurological diseases; and (f)  
CC infectious diseases such as viral, bacterial, fungal and parasitic  
CC infections. AAC74328 to AAC74336 and AAB39401 represent sequences used in  
CC the exemplification of the present invention  
XX  
XX Sequence 54 AA;  
SQ  
Query Match 98.3%; Score 170; DB 3; Length 54;  
Best Local Similarity 94.3%; Pred. No. 7.3e-18;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 LSELDDRADALQAGASXFEKSAKLRKRYWKNLK 35  
Db 20 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 54  
RESULT 6  
AAB6821  
ID AAB6821 standard; peptide; 62 AA.  
XX  
XX AAB6821;  
XX  
XX 15-AUG-1996 (first entry)  
XX  
XX VAMP isoform-1 residues 33-94.  
XX  
XX VAMP; vesicle-associated membrane protein; SNAP-25; syntaxin;  
KW neurotransmitter; neurotoxin; botulinum; botulism; cleavage; substrate;  
KW antibody; detection; assay.  
XX  
XX Synthetic.  
XX  
XX WO9533850-A1.  
XX  
XX 14-DEC-1995.  
XX  
XX 02-JUN-1995; 95WO-GB001279.  
XX  
XX 03-JUN-1994; 94GB-00011138.  
PR

XX (MICR-) MICROBIOLOGICAL RES AUTHORITY.  
 PA (CAMR-) CAMR CENT APPLIED MICROBIOLOGY & RES.  
 XX

PI Shone CC, Hallis B, James BAF, Quinn CP;  
 XX WPI, 1996-040249/04.  
 DR

XX Assay for botulinum or tetanus toxin - by combining test cpi. with  
 PT substrate which is cleaved by the toxin, and antibody specific for the  
 PT cleaved but not uncleaved substrate.  
 XX

PS Example 3; Page 28; 48pp; English.

XX The botulinum neurotoxin possesses highly specific zinc-endopeptidase  
 CC activities within their light sub-units. Depending on the neurotoxin type  
 CC these act to cleave small proteins within the nerve cell which are  
 CC involved in neurotransmitter release. Antibodies are used in assays which  
 CC detect cleaved but not uncleaved substrate. Tetanus toxin cleaves the  
 CC protein VAMP (vesicle-associated membrane protein) at an identical site  
 CC to that of botulinum toxin type B (BoNT/B). The specificities of the  
 CC endopeptidase activities of the two toxins however differ in the minimum  
 CC peptide substrate size required for cleavage. While BoNT/B requires  
 CC peptide substrates of 30-35 residues in length for optimal cleavage, the  
 CC requirement for tetanus toxin is peptide substrates of >50 residues in  
 CC length. The present sequence, VAMP isoform-1 residues 33-94, is a  
 CC suitable substrate for tetanus toxin  
 CC

SO Sequence 62 AA;

XX Query Match 98.3%; Score 170; DB 2; Length 62;  
 XX Best Local Similarity 94.3%; Pred. No. 8,6e-18;  
 XX Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXPEXSAAKLKRYKWKXK 35  
 DB 28 LSELDDRADALQAGASQFESSAAKLKRYKWKXK 62

XX RESULT 7  
 XX ADE57598  
 XX ADE57598 standard; protein; 115 AA.  
 AC

XX ADE57598;  
 XX 29-JAN-2004 (first entry)  
 XX Human Protein P19065, SEQ ID NO 3460.  
 DE

XX Human; pain; neuronal tissue; gene therapy;  
 KM spinal segmental nerve injury; chronic constriction injury; CCI;  
 KM spared nerve injury; SNI; Chung.  
 XX

OS Homo sapiens.  
 XX  
 XX MO2003016475-A2.  
 PN

XX 27-FEB-2003.  
 PD

XX 14-AUG-2002; 2002WO-US025765.  
 PF

XX 14-AUG-2001; 2001US-0312147P.  
 PR 01-NOV-2001; 2001US-0346382P.  
 PR 26-NOV-2001; 2001US-0333477P.  
 XX

XX (GEHO ) GEN HOSPITAL CORP.  
 PA (FARB ) BAYER AG.  
 XX

PI Woolf C, D'urso D, Befort K, Costigan M;  
 XX WPI, 2003-268312/26.  
 DR GENEBANK; P19065.  
 XX

PT New composition comprising two or more isolated polypeptides, useful for  
 PT preparing a medicament for treating pain in an animal.  
 XX

PS Claim 1; Page; 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat  
 CC or human polynucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC claimed are a vector comprising the novel polynucleotide, a host cell  
 CC comprising the vector, a method for identifying a nucleotide sequence  
 CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying an agent  
 CC that increases or decreases the expression of the polynucleotide sequence  
 CC that is differentially expressed in neuronal tissue of a first animal  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (SNI), chronic constriction  
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 CC therapy). The sequence presented is a human protein (shown in Table 2 of  
 CC the specification) which is differentially expressed during pain. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pcc\_sequences.  
 CC

SO Sequence 115 AA;

XX Query Match 98.3%; Score 170; DB 7; Length 115;  
 XX Best Local Similarity 94.3%; Pred. No. 1,7e-17;  
 XX Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXPEXSAAKLKRYKWKXK 35  
 DB 59 LSELDDRADALQAGASQFESSAAKLKRYKWKXK 93

XX RESULT 8  
 XX ADE57612  
 XX ADE57612 standard; protein; 115 AA.  
 AC

XX ADE57612;  
 XX

XX 29-JAN-2004 (first entry)  
 XX Rat Protein Q64357, SEQ ID NO 3474.  
 DE

XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
 KM chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
 KM  
 XX

OS Rattus norvegicus.  
 XX

XX MO2003016475-A2.  
 PN

XX 27-FEB-2003.  
 PD

XX 14-AUG-2002; 2002WO-US025765.  
 PF

XX 14-AUG-2001; 2001US-0312147P.  
 PR 01-NOV-2001; 2001US-0346382P.  
 PR 26-NOV-2001; 2001US-0333477P.  
 XX

XX (GEHO ) GEN HOSPITAL CORP.  
 PA (FARB ) BAYER AG.  
 XX

PI Woolf C, D'urso D, Befort K, Costigan M;  
 XX WPI, 2003-268312/26.  
 DR GENEBANK; P19065.  
 XX

XX WPI; 2003-266312/26.  
DR GENBANK; Q64357.  
XX  
XX  
PT New composition comprising two or more isolated polypeptides, useful for  
XX preparing a medicament for treating pain in an animal.  
XX  
XX Claim 1; Page; 1017pp; English.  
XX  
XX The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pcr\_sequences.  
XX  
SQ Sequence 115 AA;  
Query Match 98.3%; Score 170; DB 7; Length 115;  
Best Local Similarity 94.3%; Pred. No. 1.7e-17;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
CY 1 LSELDDRADALQAGASXPEXSAKLKRYKWKNLK 35  
DB 59 LSELDDRADALQAGASQFETSAAKLKRYKWKNLK 93  
RESULT 9  
ADE60831  
ID ADE60831 standard; protein; 115 AA.  
XX  
XX ADE60831;  
AC  
XX  
XX 29-JAN-2004 (first entry)  
DT  
XX  
XX Human Protein P19065, SEQ ID NO 6743.  
DE  
XX  
XX Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2003016475-A2.  
XX  
XX 27-FEB-2003.  
PD  
XX  
XX 14-AUG-2002; 2002WO-US025765.  
PF  
XX  
XX 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
PR

XX (GENO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX  
XX  
PI Woolf C, D'urso D, Befort K, Costigan M;  
XX WPI; 2003-266312/26.  
DR GENBANK; P19065.  
XX  
XX  
PT New composition comprising two or more isolated polypeptides, useful for  
XX preparing a medicament for treating pain in an animal.  
XX  
XX Claim 1; Page; 1017pp; English.  
XX  
XX The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pcr\_sequences.  
XX  
SQ Sequence 115 AA;  
Query Match 98.3%; Score 170; DB 7; Length 115;  
Best Local Similarity 94.3%; Pred. No. 1.7e-17;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
CY 1 LSELDDRADALQAGASXPEXSAKLKRYKWKNLK 35  
DB 59 LSELDDRADALQAGASQFETSAAKLKRYKWKNLK 93  
RESULT 10  
ADE57606  
ID ADE57606 standard; protein; 115 AA.  
XX  
XX ADE57606;  
AC  
XX  
XX 29-JAN-2004 (first entry)  
DT  
XX  
XX Human Protein P19065, SEQ ID NO 3468.  
DE  
XX  
XX Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.  
XX  
XX Homo sapiens.  
OS  
XX  
XX WO2003016475-A2.  
XX  
XX 27-FEB-2003.  
PD  
XX

PF 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333447P.

XX (GEHO ) GEN HOSPITAL CORP.

PA (PARB ) BAYER AG.

XX Woolf C, D'urso D, Befort K, Costigan M;

PI WPI; 2003-268312/26.

DR GENBANK; P19065.

PT New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 115 AA;

CC Query Match 98.3%; Score 170; DB 7; Length 115;  
CC Best Local Similarity 94.3%; Pred. No. 1.7e-17;  
CC Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LSELDDRADALQAGASXFEKSAKLRKRYWKNLK 35  
DB 59 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 93

RESULT 11

ADBE0829 ADE60829 standard; protein; 115 AA.

ADBE0829; (first entry)

DE 29-JAN-2004 (first entry)

XX Rat Protein Q64357, SEQ ID NO 6741.

XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

OS Rattus norvegicus.

FN W02003016475-A2.

XX 27-FEB-2003.

XX 14-AUG-2002; 2002WO-US025765.

XX 14-AUG-2001; 2001US-0312147P.

PR 01-NOV-2001; 2001US-0346382P.

PR 26-NOV-2001; 2001US-0333447P.

XX (GEHO ) GEN HOSPITAL CORP.

PA (PARB ) BAYER AG.

PT New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.

XX Claim 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene  
CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 115 AA;

CC Query Match 98.3%; Score 170; DB 7; Length 115;  
CC Best Local Similarity 94.3%; Pred. No. 1.7e-17;  
CC Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LSELDDRADALQAGASXFEKSAKLRKRYWKNLK 35  
DB 59 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 93

RESULT 12

ADBE57600 ADE57600 standard; protein; 115 AA.

ADBE57600; (first entry)

DE 29-JAN-2004 (first entry)

XX Rat Protein Q64357, SEQ ID NO 3462.

XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;

XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
 XX Rattus norvegicus.  
 XX WO2003016475-A2.  
 XX 27-FEB-2003.  
 XX 14-AUG-2002; 2002WO-US025765.  
 XX 14-AUG-2001; 2001US-0312147P.  
 XX 01-NOV-2001; 2001US-0346382P.  
 XX 26-NOV-2001; 2001US-0333347P.  
 XX (GENO) GEN HOSPITAL CORP.  
 XX (FARB) BAYER AG.  
 XX Woolf C, D'urso D, Befort K, Costigan M;  
 XX WPI; 2003-268312/26.  
 XX GENBANK; Q64357.  
 XX  
 PT New composition comprising two or more isolated polypeptides, useful for  
 PT preparing a medicament for treating pain in an animal.  
 XX  
 XX Claim 1, Page; 1017pp; English.  
 XX The invention discloses a composition comprising two or more isolated rat  
 XX or human polynucleotides or a polynucleotide which represents a fragment,  
 XX derivative or allelic variation of the nucleic acid sequence. Also  
 XX claimed are a vector comprising the novel polynucleotide, a host cell  
 XX comprising the vector, a method for identifying a nucleotide sequence  
 XX which is differentially regulated in an animal subjected to pain and a  
 XX kit to perform the method, an array, a method for identifying an agent  
 XX that increases or decreases the expression of the polynucleotide sequence  
 XX that is differentially expressed in neuronal tissue of a first animal  
 XX subjected to pain, a method for identifying a compound which regulates  
 XX the expression of a polynucleotide sequence which is differentially  
 XX expressed in an animal subjected to pain, a method for identifying a  
 XX compound that regulates the activity of one or more of the  
 XX polynucleotides, a method for producing a pharmaceutical composition, a  
 XX method for identifying a compound or small molecule that regulates the  
 XX activity in an animal of one or more of the polypeptides given in the  
 XX specification, a method for identifying a compound useful in treating  
 XX pain and a pharmaceutical composition comprising the one or more  
 XX polypeptides or their antibodies. The polynucleotide or the compound that  
 XX modulates its activity is useful for preparing a medicament for treating  
 XX pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
 XX injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene  
 XX therapy). The sequence presented is a rat protein (shown in Table 2 of  
 XX the specification) which is differentially expressed during pain. Note:  
 XX The sequence data for this patent did not form part of the printed  
 XX specification, but was obtained in electronic form directly from WIPO at  
 XX ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 XX Sequence 115 AA;  
 XX  
 XX Query Match 98.3%; Score 170; DB 7; Length 115;  
 XX Best Local Similarity 94.3%; Pred. No. 1,7e-17;  
 XX Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLRKYWKXK 35  
 Db 59 LSELDDRADALQAGASQFETSAKLRKYWKXK 93

RESULT 13  
 ADE57604  
 ID ADE57604 standard; protein; 115 AA.  
 XX ADE57604;  
 AC ADE57604;  
 XX  
 XX 29-JAN-2004 (first entry)  
 DT

XX Rat Protein Q64357, SEQ ID NO 3466.  
 XX  
 XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
 XX chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
 XX Rattus norvegicus.  
 XX WO2003016475-A2.  
 XX 27-FEB-2003.  
 XX 14-AUG-2002; 2002WO-US025765.  
 XX 14-AUG-2001; 2001US-0312147P.  
 XX 01-NOV-2001; 2001US-0346382P.  
 XX 26-NOV-2001; 2001US-0333347P.  
 XX (GENO) GEN HOSPITAL CORP.  
 XX (FARB) BAYER AG.  
 XX Woolf C, D'urso D, Befort K, Costigan M;  
 XX WPI; 2003-268312/26.  
 XX GENBANK; Q64357.  
 XX  
 PT New composition comprising two or more isolated polypeptides, useful for  
 PT preparing a medicament for treating pain in an animal.  
 XX  
 XX Claim 1, Page; 1017pp; English.  
 XX The invention discloses a composition comprising two or more isolated rat  
 XX or human polynucleotides or a polynucleotide which represents a fragment,  
 XX derivative or allelic variation of the nucleic acid sequence. Also  
 XX claimed are a vector comprising the novel polynucleotide, a host cell  
 XX comprising the vector, a method for identifying a nucleotide sequence  
 XX which is differentially regulated in an animal subjected to pain and a  
 XX kit to perform the method, an array, a method for identifying an agent  
 XX that increases or decreases the expression of the polynucleotide sequence  
 XX that is differentially expressed in neuronal tissue of a first animal  
 XX subjected to pain, a method for identifying a compound which regulates  
 XX the expression of a polynucleotide sequence which is differentially  
 XX expressed in an animal subjected to pain, a method for identifying a  
 XX compound that regulates the activity of one or more of the  
 XX polynucleotides, a method for producing a pharmaceutical composition, a  
 XX method for identifying a compound or small molecule that regulates the  
 XX activity in an animal of one or more of the polypeptides given in the  
 XX specification, a method for identifying a compound useful in treating  
 XX pain and a pharmaceutical composition comprising the one or more  
 XX polypeptides or their antibodies. The polynucleotide or the compound that  
 XX modulates its activity is useful for preparing a medicament for treating  
 XX pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
 XX injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene  
 XX therapy). The sequence presented is a rat protein (shown in Table 2 of  
 XX the specification) which is differentially expressed during pain. Note:  
 XX The sequence data for this patent did not form part of the printed  
 XX specification, but was obtained in electronic form directly from WIPO at  
 XX ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 XX Sequence 115 AA;  
 XX  
 XX Query Match 98.3%; Score 170; DB 7; Length 115;  
 XX Best Local Similarity 94.3%; Pred. No. 1,7e-17;  
 XX Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLRKYWKXK 35  
 Db 59 LSELDDRADALQAGASQFETSAKLRKYWKXK 93

RESULT 14  
 ADE57596  
 ID ADE57596 standard; protein; 115 AA.  
 DT

AC ADE57596;  
DE 29-JAN-2004 (first entry)  
DE Rat Protein Q64357, SEQ ID NO 3458.  
KM Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
KM chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
OS Rattus norvegicus.  
PN WO2003016475-A2.  
PD 27-FEB-2003.  
PF 14-AUG-2002; 2002W0-US025765.  
PR 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
PA (GENO ) GEN HOSPITAL CORP.  
PA (PARB ) BAYER AG.  
PI Woolf C, D'Urso D, Befort K, Costigan M;  
XX WPI; 2003-268312/26.  
XX GENBANK; Q64357.  
XX  
XX New composition comprising two or more isolated polypeptides, useful for  
XX preparing a medicament for treating pain in an animal.  
XX  
XX Claim 1; Page; 1017pp; English.  
XX  
XX The invention discloses a composition comprising two or more isolated rat  
XX or human polynucleotides or a polynucleotide which represents a fragment,  
XX derivative or allelic variation of the nucleic acid sequence. Also  
XX claimed are a vector comprising the novel polynucleotide, a host cell  
XX comprising the vector, a method for identifying a nucleotide sequence  
XX which is differentially regulated in an animal subjected to pain and a  
XX kit to perform the method, an array, a method for identifying an agent  
XX that increases or decreases the expression of the polynucleotide sequence  
XX that is differentially expressed in neuronal tissue of a first animal  
XX subjected to pain, a method for identifying a compound which regulates  
XX the expression of a polynucleotide sequence which is differentially  
XX expressed in an animal subjected to pain, a method for identifying a  
XX compound that regulates the activity of one or more of the  
XX polynucleotides, a method for producing a pharmaceutical composition, a  
XX method for identifying a compound or small molecule that regulates the  
XX activity in an animal of one or more of the polypeptides given in the  
XX specification, a method for identifying a compound useful in treating  
XX pain and a pharmaceutical composition comprising the one or more  
XX polypeptides or their antibodies. The polynucleotide or the compound that  
XX modulates its activity is useful for preparing a medicament for treating  
XX pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
XX therapy). The sequence presented is a rat protein (shown in Table 2 of  
XX the specification) which is differentially expressed during pain. Note:  
XX The sequence data for this patent did not form part of the printed  
XX specification, but was obtained in electronic form directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
XX Sequence 115 AA:

Query Match	98.3%;	Score 170;	DB 7;	length 115;
Best Local Similarity	94.3%;	Pred. No. 1.7e-17;		
Matches 33; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0

Qy 1 LSELDDADALQAGASQFEKSAKTKRKRYWKNLK 35  
Db 59 LSELDDADALQAGASQFEKSAKTKRKRYWKNLK 93

Matches	33;	Conservative	0;	Mismatches	2;	Indels	0;	Gaps	0;
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RESULT 15  
ID ADE57602 standard; protein, 115 AA.  
XX ADE57602;  
AC ADE57602;  
XX 29-JAN-2004 (first entry)  
XX  
XX Human Protein P19065, SEQ ID NO 3464.  
XX  
XX Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.  
XX  
XX Homo sapiens.  
OS  
XX  
XX MO2003016475-A2.  
FN  
XX  
XX 27-FEB-2003.  
FD  
XX  
XX 14-AUG-2002; 2002WO-US025765.  
PF  
XX  
XX 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
FR  
XX  
XX (GENO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX  
XX Woolf C, D'Urso D, Befort K, Costigan M;  
PI WPI; 2003-268312/26.  
DR GENEANK; P19065.  
XX  
XX  
XX New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
PT  
XX  
XX Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat or human polynucleotides or a polynucleotide which represents a fragment, derivative or allelic variation of the nucleic acid sequence. Also claimed are a vector comprising the novel polynucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence which is differentially regulated in an animal subjected to pain and a kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence that is differentially expressed in neuronal tissue of a first animal subjected to pain, a method for identifying a compound which regulates the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound or small molecule that regulates the activity in an animal of one or more of the polypeptides given in the specification, a method for identifying a compound useful in treating pain and a pharmaceutical composition comprising the one or more polypeptides or their antibodies. The polynucleotide or the compound that modulates its activity is useful for preparing a medicament for treating pain (e.g. spinal segmental nerve injury (SNI)), chronic constriction injury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene therapy). The sequence presented is a human protein (shown in Table 2 of the specification) which is differentially expressed during pain. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic form directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.

Query Match	98.3%	Score 170;	DB 7;	length 115;
Best Local Similarity	94.3%;	Pred. No. 1.7e-17;		
Matches 33; Conservative	0;	Mismatches 2;	Indels 0;	Gaps 0;

Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Tue Nov 2 10:45:13 2004

us-10-802-574-4.rag

Qy 1 LSELDDRADALQAGSXFEXSAKLRKXYWKYLK 35  
Db 59 LSELDDRADALQAGSQFETSAKLRKXYWKYLK 93

Search completed: November 1, 2004, 18:04:03  
Job time : 90 secs





Tue Nov 2 10:45:13 2004

us-10-802-574-4.ra1

Page 1

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2004, 17:53:05 ; Search time 23.4375 Seconds  
(without alignments)  
99.035 Million cell updates/sec

Title: US-10-802-574-4

Sequence: 1 LSEIDRADALQAGASXFEKSAKLKRRYMKLIK 35

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 segs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

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2: /cgn2\_6/ptodata/1/aa/5B.COMB.pep.\*  
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4: /cgn2\_6/ptodata/1/aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/1/aa/PCUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/1/aa/backfile1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	170	98.3	35	2	US-08-760-001-9
2	170	98.3	35	2	US-08-760-001-11
3	170	98.3	35	3	US-09-015-960-9
4	170	98.3	35	3	US-09-015-960-11
5	170	98.3	35	3	US-09-534-572-9
6	170	98.3	35	3	US-09-534-572-11
7	170	98.3	40	4	US-09-570-023-16
8	170	98.3	40	4	US-09-570-023-8
9	170	98.3	42	4	US-09-962-3608-9
10	170	98.3	62	2	US-08-760-001-8
11	170	98.3	62	2	US-09-015-960-8
12	170	98.3	62	3	US-09-534-572-8
13	170	98.3	116	1	US-08-409-373B-4
14	170	98.3	116	1	US-08-409-373B-4
15	170	98.3	116	1	US-08-393-985-16
16	170	98.3	116	3	US-08-621-018B-10
17	170	98.3	116	3	US-08-819-286-2
18	170	98.3	116	4	US-09-483-665-10
19	169	97.7	35	4	US-09-962-3608-4
20	168	97.1	82	4	US-08-621-018B-11
21	168	97.1	82	4	US-09-483-665-11
22	165	95.4	100	3	US-08-621-018B-6
23	165	95.4	100	4	US-09-483-665-6
24	165	95.4	103	1	US-08-409-373B-3
25	165	95.4	103	1	US-08-409-373B-3
26	165	95.4	103	3	US-08-621-018B-9
27	165	95.4	103	4	US-09-483-665-9

28	165	95.4	118	1	US-08-393-985-14	Sequence 14, Appl
29	165	95.4	347	4	US-09-513-783A-28	Sequence 28, Appl
30	165	95.4	447	4	US-09-430-656-30	Sequence 30, Appl
31	165	95.4	350	4	US-09-513-783A-30	Sequence 30, Appl
32	165	95.4	350	4	US-09-430-656-28	Sequence 28, Appl
33	162	93.6	35	4	US-09-962-3608-3	Sequence 3, Appl
34	106	61.3	56	3	US-08-819-286-5	Sequence 5, Appl
35	93	53.8	94	4	US-09-621-976-6274	Sequence 6274, Ap
36	82	47.4	20	3	US-08-819-286-13	Sequence 13, Appl
37	82	47.4	71	4	US-09-621-976-5656	Sequence 5656, Ap
38	82	47.4	86	4	US-09-513-999C-5451	Sequence 5451, Ap
39	82	47.4	102	1	US-08-409-373B-2	Sequence 2, Appl
40	82	47.4	102	1	US-08-409-373B-2	Sequence 2, Appl
41	82	47.4	102	3	US-08-621-018B-2	Sequence 2, Appl
42	82	47.4	102	4	US-08-483-665-2	Sequence 2, Appl
43	76	43.9	141	3	US-08-621-018B-8	Sequence 8, Appl
44	76	43.9	141	4	US-09-483-665-8	Sequence 8, Appl
45	75	43.4	46	4	US-09-962-3608-10	Sequence 10, Appl

#### ALIGNMENTS

RESULT 1  
US-08-760-001-9  
Sequence 9, Application US/08760001  
Patent No. 5962637  
GENERAL INFORMATION:  
APPLICANT: Stone, Clifford C.  
APPLICANT: Hallis, Bassam  
APPLICANT: James, Benjamin A. F.  
APPLICANT: Quinn, Conrad P.  
TITLE OF INVENTION: TOXIN ASSAY  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/760,001  
FILING DATE: Herewith  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB95/01279  
FILING DATE: 02-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1581.0120001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2543  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-760-001-9  
Query Match 98.3%; Score 170; DB 2; Length 35;  
Best Local Similarity 94.3%; Pred. No. 3,7e-19;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLRKRYWKNLK 35  
DB 1 LSELDDRADALQAGASQFESSAKLRKRYWKNLK 35

## RESULT 2

US-08-760-001-11  
Sequence 11, Application US/08760001

Patent No. 5962637

GENERAL INFORMATION:

APPLICANT: Shone, Clifford C.

APPLICANT: Hallis, Bassam

APPLICANT: James, Benjamin A. F.

APPLICANT: Quinn, Conrad P.

TITLE OF INVENTION: TOXIN ASSAY

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

STREET: 1100 New York Ave., N.W., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/760,001

FILING DATE: Herewith

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/GB95/01279

FILING DATE: 02-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 1581.0120001

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2543

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 35 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-760-001-11

Query Match

Best Local Similarity 98.3%; Score 170; DB 2; Length 35;

Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

US-09-015-960-9

Sequence 9, Application US/09015960

Patent No. 6043042

GENERAL INFORMATION:

APPLICANT: Shone, Clifford C.

APPLICANT: Hallis, Bassam

APPLICANT: James, Benjamin A. F.

APPLICANT: Quinn, Conrad P.

TITLE OF INVENTION: TOXIN ASSAY

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

STREET: 1100 New York Ave., N.W., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/015,960

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/760,001

FILING DATE:

ATTORNEY/AGENT INFORMATION:

STREET: 1100 New York Ave., N.W., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/015,960

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/760,001

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: Esmond, Robert W.

REGISTRATION NUMBER: 32,893

REFERENCE/DOCKET NUMBER: 1581.0120001

TELEPHONE: 202-371-2600

TELEFAX: 202-371-2543

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 35 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-015-960-9

Query Match

Best Local Similarity 98.3%; Score 170; DB 3; Length 35;

Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

US-09-015-960-11

Sequence 11, Application US/09015960

Patent No. 6043042

GENERAL INFORMATION:

APPLICANT: Shone, Clifford C.

APPLICANT: Hallis, Bassam

APPLICANT: James, Benjamin A. F.

APPLICANT: Quinn, Conrad P.

TITLE OF INVENTION: TOXIN ASSAY

NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:

ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.

STREET: 1100 New York Ave., N.W., Suite 600

CITY: Washington

STATE: DC

COUNTRY: USA

ZIP: 20005-3934

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/015,960

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/760,001

FILING DATE:

ATTORNEY/AGENT INFORMATION:

Tue Nov 2 10:45:13 2004

US-10-802-574-4.ra1

Page 3

NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1581.0120001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2543  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-015-960-11

Query Match 98.3%; Score 170; DB 3; Length 35;  
Best Local Similarity 94.3%; Pred. No. 3.7e-19;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDPRADALQAGASXFEKSAKLRKYWKXNLK 35  
Db 1 LSELDPRADALQAGASQFETSAAKLRKYWKXNLK 35

RESULT 5  
US-09-534-572-9  
Sequence 9, Application US/09534572  
Patent No. 6337386  
GENERAL INFORMATION:  
APPLICANT: Shone, Clifford C.  
APPLICANT: Hallis, Bassam  
APPLICANT: James, Benjamin A. F.  
APPLICANT: Quinn, Conrad P.  
TITLE OF INVENTION: TOXIN ASSAY  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/534,572  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/015,960  
FILING DATE: 30-JAN-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/760,001  
FILING DATE: 30-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB95/01279  
FILING DATE: 02-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1581.0120003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2543  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: peptide  
US-09-534-572-9

Query Match 98.3%; Score 170; DB 3; Length 35;  
Best Local Similarity 94.3%; Pred. No. 3.7e-19;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDPRADALQAGASXFEKSAKLRKYWKXNLK 35  
Db 1 LSELDPRADALQAGASQFETSAAKLRKYWKXNLK 35

RESULT 6  
US-09-534-572-11  
Sequence 11, Application US/09534572  
Patent No. 6337386  
GENERAL INFORMATION:  
APPLICANT: Shone, Clifford C.  
APPLICANT: Hallis, Bassam  
APPLICANT: James, Benjamin A. F.  
APPLICANT: Quinn, Conrad P.  
TITLE OF INVENTION: TOXIN ASSAY  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/534,572  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/015,960  
FILING DATE: 30-JAN-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/760,001  
FILING DATE: 30-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB95/01279  
FILING DATE: 02-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1581.0120003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2543  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-534-572-11

Query Match 98.3%; Score 170; DB 3; Length 35;  
Best Local Similarity 94.3%; Pred. No. 3.7e-19;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSELDPRADALQAGASXFEKSAKLRKYWKXNLK 35  
Db 1 LSELDPRADALQAGASQFETSAAKLRKYWKXNLK 35

RESULT 7  
US-09-570-022-16  
Sequence 16, Application US/09570022  
Patent No. 6573244  
GENERAL INFORMATION:  
APPLICANT: GORDON, RICHARD K.  
APPLICANT: MOORAD, DEBORAH R.  
APPLICANT: DOCTOR, BHUPENDRA P.  
APPLICANT: GARCIA, GREGORY E.  
TITLE OF INVENTION: PREVINS AS SPECIFIC INHIBITORS AND THERAPEUTIC AGENTS  
FILE REFERENCE: 38644-170531  
CURRENT APPLICATION NUMBER: US/09/570,022  
CURRENT FILING DATE: 2000-05-12  
PRIOR APPLICATION NUMBER: 60/134,446  
PRIOR FILING DATE: 1999-05-17  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 16  
LENGTH: 40  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-570-022-16

Query Match 98.3%; Score 170; DB 4; Length 40;  
Best Local Similarity 94.3%; Pred. No. 4.3e-19;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 LSELDDRADALQAGASQFETSAAKLRKRYWKNLK 35  
6 LSELDDRADALQAGASQFETSAAKLRKRYWKNLK 40

RESULT 8  
US-09-570-023-8  
Sequence 8, Application US/09570023  
Patent No. 6713444  
GENERAL INFORMATION:  
APPLICANT: GARCIA, GREGORY E.  
APPLICANT: GORDON, RICHARD K.  
APPLICANT: MOORAD, DEBORAH R.  
APPLICANT: DOCTOR, BHUPENDRA P.  
TITLE OF INVENTION: BOTULINUM TOXIN B AND TETANUS NEUROTOXINS  
FILE REFERENCE: 37833-20004-00  
CURRENT APPLICATION NUMBER: US/09/570,023  
CURRENT FILING DATE: 2000-05-12  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 8  
LENGTH: 40  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
OTHER INFORMATION: VAMP2  
US-09-570-023-8

Query Match 98.3%; Score 170; DB 4; Length 40;  
Best Local Similarity 94.3%; Pred. No. 4.3e-19;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 LSELDDRADALQAGASQFETSAAKLRKRYWKNLK 35  
6 LSELDDRADALQAGASQFETSAAKLRKRYWKNLK 40

RESULT 9  
US-09-962-360B-9  
Sequence 9, Application US/09962360B  
Patent No. 6762280  
GENERAL INFORMATION:  
/9

APPLICANT: Schmidt, James J.  
APPLICANT: Stafford, Robert G.  
TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi  
FILE REFERENCE: 003/224/SAP  
CURRENT APPLICATION NUMBER: US/09/962,360B  
CURRENT FILING DATE: 2002-08-19  
PRIOR APPLICATION NUMBER: US 60/235,050  
PRIOR FILING DATE: 2001-09-25  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: Apple Macintosh Microsoft Word 6.0  
SEQ ID NO 9  
LENGTH: 42  
TYPE: PRT  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BONT B  
NAME/KEY: misc\_feature  
LOCATION: 1  
OTHER INFORMATION: Xaa at 1 is N-fluoresceinyl-glycine  
US-09-962-360B-9

Query Match 98.3%; Score 170; DB 4; Length 42;  
Best Local Similarity 94.3%; Pred. No. 4.6e-19;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 LSELDDRADALQAGASQFETSAAKLRKRYWKNLK 35  
4 LSELDDRADALQAGASQFETSAAKLRKRYWKNLK 38

RESULT 10  
US-08-760-001-8  
Sequence 8, Application US/08760001  
Patent No. 5962637  
GENERAL INFORMATION:  
APPLICANT: Shone, Clifford C.  
APPLICANT: Hallie, Bassam  
APPLICANT: James, Benjamin A. F.  
APPLICANT: Quinn, Conrad P.  
TITLE OF INVENTION: TOXIN ASSAY  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/760,001  
FILING DATE: Herewith  
CLASSIFICATION: 510  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB95/01279  
FILING DATE: 02-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,693  
REFERENCE/DOCKET NUMBER: 1581.0120001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2543  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 62 amino acids  
TYPE: amino acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-760-001-8

Query Match 98.3%; Score 170; DB 2; Length 62;  
Best Local Similarity 94.3%; Pred. No. 7.1e-19;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLRKRYWKNLK 35  
DB 28 LSELDDRADALQAGASQFESSAKLRKRYWKNLK 62

RESULT 11  
US-09-015-960-8  
Sequence 8, Application US/09015960  
Patent No. 6043042  
GENERAL INFORMATION:  
APPLICANT: Shone, Clifford C.  
APPLICANT: Hallis, Bassam  
APPLICANT: James, Benjamin A. F.  
APPLICANT: Quinn, Conrad P.  
TITLE OF INVENTION: TOXIN ASSAY  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/015,960  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/760,001  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1581.0120001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2543  
TELEFAX: 202-371-2543  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 62 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-015-960-8

Query Match 98.3%; Score 170; DB 3; Length 62;  
Best Local Similarity 94.3%; Pred. No. 7.1e-19;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLRKRYWKNLK 35  
DB 28 LSELDDRADALQAGASQFESSAKLRKRYWKNLK 62

RESULT 12  
US-09-534-572-8  
Sequence 8, Application US/09534572  
Patent No. 6337386

GENERAL INFORMATION:  
APPLICANT: Shone, Clifford C.  
APPLICANT: Hallis, Bassam  
APPLICANT: James, Benjamin A. F.  
APPLICANT: Quinn, Conrad P.  
TITLE OF INVENTION: TOXIN ASSAY  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/534,572  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/015,960  
FILING DATE: 30-JAN-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/760,001  
FILING DATE: 30-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB95/01279  
FILING DATE: 02-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1581.0120003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2543  
TELEFAX: 202-371-2543  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 62 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-534-572-8

Query Match 98.3%; Score 170; DB 3; Length 62;  
Best Local Similarity 94.3%; Pred. No. 7.1e-19;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLRKRYWKNLK 35  
DB 28 LSELDDRADALQAGASQFESSAKLRKRYWKNLK 62

RESULT 13  
US-08-409-373B-4  
Sequence 4, Application US/08409373B  
Patent No. 5585240  
GENERAL INFORMATION:  
APPLICANT: Stuart, Susan G.  
APPLICANT: Hawkins, Phillip R.  
APPLICANT: Seilhamer, Jeffrey J.  
TITLE OF INVENTION: CELLULEREVIN HOMOLOG  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.

ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/409,373B  
FILING DATE: 23-MAR-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J.  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0029 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 116 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: X76199  
US-08-409-373B-4

Query Match 98.3%; Score 170; DB 1; Length 116;  
Best Local Similarity 94.3%; Pred. No. 1.5e-18;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 35  
Db 60 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 94

RESULT 14  
US-08-409-373B-4  
Sequence 4, Application US/08409373B  
Patent No. 5650280 5585240  
GENERAL INFORMATION:  
APPLICANT: Stuart, Susan G.  
APPLICANT: Hawkins, Phillip R.  
APPLICANT: Sellhauer, Jeffrey J.  
TITLE OF INVENTION: CELLUBREVIN HOMOLOG  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/409,373B  
FILING DATE: 23-MAR-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J.  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0029 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:  
LENGTH: 116 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: X76199  
US-08-409-373B-4

Query Match 98.3%; Score 170; DB 1; Length 116;  
Best Local Similarity 94.3%; Pred. No. 1.5e-18;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 35  
Db 60 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 94

RESULT 15  
US-08-393-985-16  
Sequence 16, Application US/08393985  
Patent No. 5693476  
GENERAL INFORMATION:  
APPLICANT: Scheller, Richard H.  
TITLE OF INVENTION: Methods and Compositions for Modulation  
of Vesicular Release  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: 350 Cambridge Avenue, Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/393,985  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Sholtz, Charles K.  
REGISTRATION NUMBER: 38,615  
REFERENCE/DOCKET NUMBER: 8600-0152  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 116 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-393-985-16

Query Match 98.3%; Score 170; DB 1; Length 116;  
Best Local Similarity 94.3%; Pred. No. 1.5e-18;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 35  
Db 60 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 94

Search completed: November 1, 2004, 18:19:41  
Job time : 23.4375 secs

Tue Nov 2 10:45:13 2004

us-10-802-574-4.rapb

Page 1

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OM protein - protein search, using sw model

Run on: November 1, 2004, 17:59:20 ; Search time 69.0625 Seconds  
(without alignments)  
164.308 Million cell updates/sec

Title: US-10-802-574-4

Perfect score: 173  
Sequence: 1 LSELDPRADALQAGASXFEKSAKLRKRWKXK 35

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: Published Applications AA:  
1: /cgn2\_6/ptodata/2/pubppaa/US07\_PUBCOMB.pep.\*  
2: /cgn2\_6/ptodata/2/pubppaa/US06\_PUB\_PUB.pep.\*  
3: /cgn2\_6/ptodata/2/pubppaa/US06\_PUB\_PUB.pep.\*  
4: /cgn2\_6/ptodata/2/pubppaa/US06\_PUBCOMB.pep.\*  
5: /cgn2\_6/ptodata/2/pubppaa/US07\_PUB\_PUB.pep.\*  
6: /cgn2\_6/ptodata/2/pubppaa/US07\_PUBCOMB.pep.\*  
7: /cgn2\_6/ptodata/2/pubppaa/US08\_PUB\_PUB.pep.\*  
8: /cgn2\_6/ptodata/2/pubppaa/US08\_PUBCOMB.pep.\*  
9: /cgn2\_6/ptodata/2/pubppaa/US09\_PUBCOMB.pep.\*  
10: /cgn2\_6/ptodata/2/pubppaa/US09\_PUBCOMB.pep.\*  
11: /cgn2\_6/ptodata/2/pubppaa/US09\_PUB\_PUB.pep.\*  
12: /cgn2\_6/ptodata/2/pubppaa/US09\_PUB\_PUB.pep.\*  
13: /cgn2\_6/ptodata/2/pubppaa/US10\_PUBCOMB.pep.\*  
14: /cgn2\_6/ptodata/2/pubppaa/US10\_PUBCOMB.pep.\*  
15: /cgn2\_6/ptodata/2/pubppaa/US10\_PUBCOMB.pep.\*  
16: /cgn2\_6/ptodata/2/pubppaa/US10\_PUBCOMB.pep.\*  
17: /cgn2\_6/ptodata/2/pubppaa/US10\_PUB\_PUB.pep.\*  
18: /cgn2\_6/ptodata/2/pubppaa/US10\_PUB\_PUB.pep.\*  
19: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep.\*  
20: /cgn2\_6/ptodata/2/pubppaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	170	98.3	42	US-09-962-360B-9	Sequence 9, Appl1
2	170	98.3	116	US-09-942-024-4	Sequence 4, Appl1
3	170	98.3	116	US-09-942-024-17	Sequence 17, Appl1
4	170	98.3	116	US-09-942-024-18	Sequence 18, Appl1
5	170	98.3	116	US-09-942-024-18	Sequence 18, Appl1
6	170	98.3	116	US-09-942-024-18	Sequence 17, Appl1
7	170	98.3	116	US-09-942-024-18	Sequence 16, Appl1
8	170	98.3	116	US-09-942-024-18	Sequence 15, Appl1
9	170	98.3	116	US-09-942-024-18	Sequence 14, Appl1
10	170	98.3	116	US-09-942-024-18	Sequence 13, Appl1
11	170	98.3	116	US-09-942-024-18	Sequence 12, Appl1
12	170	98.3	116	US-09-942-024-18	Sequence 11, Appl1
13	169	97.7	35	US-09-962-360B-4	Sequence 4, Appl1

14	168	97.1	82	US-10-357-028-11	Sequence 11, Appl1
15	168	97.1	114	US-09-942-024-19	Sequence 19, Appl1
16	168	97.1	114	US-09-942-024-19	Sequence 19, Appl1
17	168	97.1	114	US-10-261-161-14	Sequence 14, Appl1
18	165	95.4	103	US-10-357-028-6	Sequence 6, Appl1
19	165	95.4	103	US-10-357-028-6	Sequence 9, Appl1
20	165	95.4	117	US-10-467-595-27	Sequence 27, Appl1
21	165	95.4	118	US-09-942-024-96	Sequence 96, Appl1
22	165	95.4	118	US-09-942-024-96	Sequence 96, Appl1
23	165	95.4	118	US-10-261-161-10	Sequence 10, Appl1
24	165	95.4	347	US-10-100-9578-28	Sequence 28, Appl1
25	165	95.4	350	US-10-100-9578-30	Sequence 30, Appl1
26	165	95.4	365	US-09-293-670-52	Sequence 52, Appl1
27	162	93.6	35	US-09-962-360B-3	Sequence 3, Appl1
28	153	88.4	109	US-10-369-493-6364	Sequence 6364, Appl1
29	150	86.7	40	US-09-942-024-57	Sequence 57, Appl1
30	150	86.7	40	US-09-942-024-58	Sequence 58, Appl1
31	150	86.7	40	US-09-942-024-59	Sequence 59, Appl1
32	150	86.7	40	US-09-942-024-60	Sequence 60, Appl1
33	150	86.7	40	US-09-942-024-61	Sequence 61, Appl1
34	150	86.7	40	US-09-942-024-65	Sequence 65, Appl1
35	150	86.7	40	US-09-942-024-65	Sequence 65, Appl1
36	150	86.7	40	US-09-942-024-65	Sequence 58, Appl1
37	150	86.7	40	US-09-942-024-65	Sequence 58, Appl1
38	150	86.7	40	US-09-942-024-65	Sequence 60, Appl1
39	150	86.7	40	US-09-942-024-65	Sequence 61, Appl1
40	150	86.7	40	US-09-942-024-65	Sequence 61, Appl1
41	150	86.7	40	US-10-261-161-82	Sequence 82, Appl1
42	150	86.7	40	US-10-261-161-83	Sequence 83, Appl1
43	150	86.7	40	US-10-261-161-84	Sequence 84, Appl1
44	150	86.7	40	US-10-261-161-85	Sequence 85, Appl1
45	150	86.7	40	US-10-261-161-86	Sequence 86, Appl1

ALIGNMENTS

RESULT 1  
US-09-962-360B-9  
; Sequence 9, Application US/09962360B  
; Publication No. US2003077685A1  
; GENERAL INFORMATION:  
; /9  
; APPLICANT: Schmitt, James J.  
; APPLICANT: Stafford, Robert G.  
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi  
; FILE REFERENCE: 003/224/SAP  
; CURRENT APPLICATION NUMBER: US/09/962,360B  
; CURRENT FILING DATE: 2002-08-19  
; PRIOR APPLICATION NUMBER: US 60/235,050  
; PRIOR FILING DATE: 2001-09-25  
; NUMBER OF SEQ ID NOS: 12  
; SOFTWARE: Apple Macintosh Microsoft Word 6.0  
; SEQ ID NO 9  
; LENGTH: 42  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BONT B  
; NAME/KEY: misc\_feature  
; LOCATION: 1  
; OTHER INFORMATION: Xaa at 1 is N-fluoreceinyl-glycine  
US-09-962-360B-9  
Query Match 98.3%; Score 170; DB 10; Length 42;  
Best Local Similarity 98.3%; Pred. No. 2.7e-17;  
Matches 33; Conservatively 0; Mismatches 2; Indels 0; Gaps 0;  
1 LSELDPRADALQAGASXFEKSAKLRKRWKXK 35  
4 LSELDPRADALQAGASQFETSAKLRKRWKXK 38

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RESULT 2
US-09-942-024-4
; Sequence 4, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-024-4

Query Match          98.3%; Score 170; DB 10; Length 116;
Best Local Similarity 94.3%; Pred. No. 7.7e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LSELDDRADALQAGASXFEKSAKLRKRYWKNLK 35
DB 60 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 94

RESULT 3
US-09-942-024-17
; Sequence 17, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-942-024-17

Query Match          98.3%; Score 170; DB 10; Length 116;
Best Local Similarity 94.3%; Pred. No. 7.7e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LSELDDRADALQAGASXFEKSAKLRKRYWKNLK 35
DB 60 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 94

RESULT 4
US-09-942-024-18
; Sequence 18, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-942-024-18

Query Match          98.3%; Score 170; DB 10; Length 116;
Best Local Similarity 94.3%; Pred. No. 7.7e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-942-024-18

Query Match          98.3%; Score 170; DB 10; Length 116;
Best Local Similarity 94.3%; Pred. No. 7.7e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LSELDDRADALQAGASXFEKSAKLRKRYWKNLK 35
DB 60 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 94

RESULT 5
US-09-942-098-4
; Sequence 4, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-098-4

Query Match          98.3%; Score 170; DB 10; Length 116;
Best Local Similarity 94.3%; Pred. No. 7.7e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LSELDDRADALQAGASXFEKSAKLRKRYWKNLK 35
DB 60 LSELDDRADALQAGASQFETSAKLRKRYWKNLK 94

RESULT 6
US-09-942-098-17
; Sequence 17, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-942-098-17

Query Match          98.3%; Score 170; DB 10; Length 116;
Best Local Similarity 94.3%; Pred. No. 7.7e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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Tue Nov 2 10:45:13 2004

us-10-802-574-4.rapb

Page 3

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Qy      1 LSELDPRADALQAGASQFETSAAKLKRYKWKX 35
Db      60 LSELDPRADALQAGASQFETSAAKLKRYKWKX 94

RESULT 7
US-09-942-098-18
; Sequence 18, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-942-098-18

Query Match      98.3%; Score 170; DB 10; Length 116;
Best Local Similarity 94.3%; Pred. No. 7,7e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 LSELDPRADALQAGASQFETSAAKLKRYKWKX 35
Db      60 LSELDPRADALQAGASQFETSAAKLKRYKWKX 94

RESULT 8
US-10-357-028-10
; Sequence 10, Application US/10357028
; Publication No. US20030180931A1
; GENERAL INFORMATION:
; APPLICANT: Stuart, Susan G.
; APPLICANT: Hawkins, Phillip R.
; APPLICANT: Selhammer, Jeffrey J.
; APPLICANT: Murry, Lynn E.
; TITLE OF INVENTION: CELLULREVIN HOMOLOGS
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: U.S.
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/357,028
; FILING DATE: 29-Jan-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/483,665
; FILING DATE: Herewith
; APPLICATION NUMBER: 08/621,018
; FILING DATE: March 22, 1996
; APPLICATION NUMBER: 08/409,373
; FILING DATE: March 23, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Hamlet-Cox, Diana
; REGISTRATION NUMBER: 33,102
; REFERENCE/DOCKET NUMBER: PF-0029-2 DIV
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TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-855-0555
; TELEFAX: 650-849-8886
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 116 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: GI 433075
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-357-028-10

Query Match      98.3%; Score 170; DB 14; Length 116;
Best Local Similarity 94.3%; Pred. No. 7,7e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 LSELDPRADALQAGASQFETSAAKLKRYKWKX 35
Db      60 LSELDPRADALQAGASQFETSAAKLKRYKWKX 94

RESULT 9
US-10-261-161-11
; Sequence 11, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-261-161-11

Query Match      98.3%; Score 170; DB 15; Length 116;
Best Local Similarity 94.3%; Pred. No. 7,7e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      1 LSELDPRADALQAGASQFETSAAKLKRYKWKX 35
Db      60 LSELDPRADALQAGASQFETSAAKLKRYKWKX 94

RESULT 10
US-10-261-161-12
; Sequence 12, Application US/10261161
; Publication No. US20040072270A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy
; TITLE OF INVENTION: Transfer (FRET) Assays For Clostridial Toxins
; FILE REFERENCE: P-AR 4804
; CURRENT APPLICATION NUMBER: US/10/261,161
; CURRENT FILING DATE: 2002-09-27
; NUMBER OF SEQ ID NOS: 109
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 116
; TYPE: PRT
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ORGANISM: Mus musculus  
US-10-261-161-12

Query Match 98.3%; Score 170; DB 15; Length 116;  
Best Local Similarity 94.3%; Pred. No. 7.7e-17;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDPRADALQAGASXFEKSAKLRKRYWKNLK 35  
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DB 60 LSELDPRADALQAGASQFETSAKLRKRYWKNLK 94

RESULT 11  
US-10-261-161-13  
Sequence 13, Application US/10261161  
Publication No. US20040072270A1  
GENERAL INFORMATION:  
APPLICANT: Fernandez-Salas, Ester  
APPLICANT: Steward, Lance E.  
APPLICANT: Aoki, Kei Roger  
TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy  
TITLE OF INVENTION: Transfer (FRET) Assays for Clostridial Toxins  
FILE REFERENCE: P-AR 4804  
CURRENT APPLICATION NUMBER: US/10/261,161  
CURRENT FILING DATE: 2002-09-27  
NUMBER OF SEQ ID NOS: 109  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13  
LENGTH: 116  
TYPE: PRF  
ORGANISM: Bos taurus  
US-10-261-161-13

Query Match 98.3%; Score 170; DB 15; Length 116;  
Best Local Similarity 94.3%; Pred. No. 7.7e-17;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDPRADALQAGASXFEKSAKLRKRYWKNLK 35  
|||||  
DB 60 LSELDPRADALQAGASQFETSAKLRKRYWKNLK 94

RESULT 12  
US-09-293-670-55  
Sequence 55, Application US/09293670  
Publication No. US20030190684A1  
GENERAL INFORMATION:  
APPLICANT: Fisher, Joseph  
APPLICANT: Lorens, James  
APPLICANT: Payan, Donald  
TITLE OF INVENTION: Multiparameter Facs Assays to Detect Alterations in  
TITLE OF INVENTION: Cellular Parameters and to Screen Small Molecule  
FILE REFERENCE: A68104/DJB/RMS/DAV  
CURRENT APPLICATION NUMBER: US/09/293,670  
CURRENT FILING DATE: 1999-04-16  
NUMBER OF SEQ ID NOS: 57  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 55  
LENGTH: 607  
TYPE: PRF  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-293-670-55

Query Match 98.3%; Score 170; DB 10; Length 607;  
Best Local Similarity 94.3%; Pred. No. 4.3e-16;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDPRADALQAGASXFEKSAKLRKRYWKNLK 35  
|||||

DB 61 LSELDPRADALQAGASQFETSAKLRKRYWKNLK 95

RESULT 13  
US-09-962-360B-4  
Sequence 4, Application US/09962360B  
Publication No. US20030077685A1  
GENERAL INFORMATION:  
/9

APPLICANT: Schmidt, James J.  
APPLICANT: Stafford, Robert G.  
TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi  
FILE REFERENCE: 003/224/SAP  
CURRENT APPLICATION NUMBER: US/09/962,360B  
CURRENT FILING DATE: 2002-08-19  
PRIOR APPLICATION NUMBER: US 60/235,050  
PRIOR FILING DATE: 2001-09-25  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: Apple Macintosh Microsoft Word 6.0  
SEQ ID NO 4  
LENGTH: 35  
TYPE: PRF  
ORGANISM: Artificial sequence  
FEATURE:  
OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BONT B  
NAME/KEY: misc feature  
LOCATION: 17 and 20  
OTHER INFORMATION: Xaa at 17 is N(epsilon)-2,4-(dinitrophenyl)-lysine and Xaa at 20 ;  
OTHER INFORMATION: dimethylamino-4-methyl-coumarin-3-carboxamidomethyl)-cysteine  
US-09-962-360B-4

Query Match 97.7%; Score 169; DB 10; Length 35;  
Best Local Similarity 100.0%; Pred. No. 3.1e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LSELDPRADALQAGASXFEKSAKLRKRYWKNLK 35  
|||||  
DB 1 LSELDPRADALQAGASXFEKSAKLRKRYWKNLK 35

RESULT 14  
US-10-357-028-11  
Sequence 11, Application US/10357028  
Publication No. US20030180931A1  
GENERAL INFORMATION:  
APPLICANT: Stuart, Susan G.  
APPLICANT: Hawkins, Phillip R.  
APPLICANT: Selhamer, Jeffrey J.  
Murry, Lynn E.  
TITLE OF INVENTION: CELLULREVIN HOMOLOGS  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/357,028  
FILING DATE: 29-Jan-2003  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/483,665  
FILING DATE: Herewith  
APPLICATION NUMBER: 08/621,018  
FILING DATE: March 22, 1996

APPLICATION NUMBER: 08/409,373  
FILING DATE: March 23, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Hamlet-Cox, Diana  
REGISTRATION NUMBER: 33,302  
REFERENCE/DOCKET NUMBER: PF-0029-2 DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-849-8886  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 82 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: GI 606978  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-10-357-028-11

Query Match 97.1%; Score 168; DB 10; Length 82;  
Best Local Similarity 91.4%; Pred. No. 1,1e-16;  
Matches 32; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDPRADALQAGASXFEKSAKTKRKYWKNLK 35  
DB 26 LSELDPRADALQAGASQFETSAAKTKRKYWKNNK 60

RESULT 15  
US-09-942-024-19  
Sequence 19, Application US/09942024  
Publication No. US20030143650A1  
GENERAL INFORMATION:  
APPLICANT: Steward, Lance E.  
APPLICANT: Fernandez-Salas, Estel  
APPLICANT: Aoki, Kei Roger  
TITLE OF INVENTION: Pret Protease Assays For Botulinum  
TITLE OF INVENTION: Serotype A/E Toxins  
FILE REFERENCE: P-AR 4803  
CURRENT APPLICATION NUMBER: US/09/942,024  
CURRENT FILING DATE: 2001-08-28  
NUMBER OF SEQ ID NOS: 96  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 19  
LENGTH: 114  
TYPE: PRT  
ORGANISM: Xenopus laevis  
US-09-942-024-19

Query Match 97.1%; Score 168; DB 10; Length 114;  
Best Local Similarity 91.4%; Pred. No. 1.5e-16;  
Matches 32; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDPRADALQAGASXFEKSAKTKRKYWKNLK 35  
DB 58 LSELDPRADALQAGASQFETSAAKTKRKYWKNNK 92

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Job time : 69.0625 secs



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 1, 2004, 17:52:25 / Search time 18.125 Seconds  
(without alignments)  
185.798 Million cell updates/sec

Title: US-10-802-574-4  
Perfect score: 173  
Sequence: 1 LSELDRADALQAGASXFEKSAKLRKRWKNLK 35

Scoring table: BLOSUM62  
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: PIR.79:\*  
2: PIR1:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	170	98.3	116	2	B38315 synaptobrevin 2 -
2	170	98.3	116	2	UN0011 synaptobrevin 2 -
3	170	98.3	116	2	B34288 synaptobrevin 2 -
4	165	95.4	103	2	B35077 cellubrevin - rat
5	165	95.4	118	2	S52747 Vamp1 protein - hu
6	165	95.4	118	2	A38315 synaptobrevin 1 -
7	165	95.4	118	2	A34288 vesicle-associated
8	165	95.4	120	2	A32146 vesicle-associated
9	155	89.6	125	2	S40153 synaptobrevin - lo
10	153	88.4	109	2	T33239 synaptobrevin SNB-
11	116	67.1	32	2	S35553 vesicle-associated
12	116	67.1	32	2	S35553 vesicle-associated
13	116	67.1	32	2	S35554 vesicle-associated
14	116	67.1	32	2	S35552 vesicle-associated
15	113	65.3	132	2	JC1522 synaptobrevin 1sof
16	113	65.3	132	2	UC1521 synaptobrevin 1sof
17	107	61.8	145	2	T13138 synaptobrevin prote
18	82	47.4	115	2	T13138 synaptobrevin homo
19	81	46.8	123	2	S47654 integral membrane
20	76	43.9	121	2	T39073 synaptobrevin homo
21	72	41.6	117	2	S31250 synaptobrevin homo
22	71	41.0	1237	1	GNPFA2 HIV-1 retropepsin
23	66	38.2	220	2	T00801 probable synaptoch
24	62	35.8	60	2	D44088 homeotic protein H
25	62	35.8	221	2	F84741 probable synaptoch
26	60	34.7	151	2	D86180 hypothetical prote
27	57	33.9	251	2	S64927 probable membrane
28	57	33.9	663	2	H87731 glutaryl-7-ACA acy
29	56	32.4	229	2	F66180 hypothetical prote

30	56	32.4	240	2	T47589 synaptobrevin-like
31	55	31.8	102	2	S44781 C30A5.4 protein -
32	55	31.8	102	2	T24909 hypothetical prote
33	54	31.2	219	2	T04630 synaptobrevin homo
34	54	31.2	226	2	A97774 p62r protein [mpo
35	54	31.2	499	2	T18791 gamma-aminobutyric
36	53	30.6	259	2	A83377 cell division prot
37	53	30.6	450	2	A97740 hypothetical prote
38	53	30.6	450	2	A71678 probable response
39	52	30.1	855	2	T29775 hypothetical prote
40	52	30.1	1116	2	T42213 m-tomoxyn, isoform
41	51	29.5	210	2	T16595 hypothetical prote
42	51	29.5	1882	2	S73484 hypothetical prote
43	50	28.9	251	2	AD1145 cyclase Hsf homol
44	50	28.9	629	2	E64046 mismatch repair pr
45	50	28.9	958	2	S15566 pol protein - siml

## ALIGNMENTS

RESULT 1  
B38315  
synaptobrevin 2 - human  
C:Species: Homo sapiens (man)  
C>Date: 14-Jun-1991 #sequence\_revision 14-Jun-1991 #text\_change 09-Jul-2004  
C/Accession: B38315  
R/Archer III, B.T.; Oerzelik, T.; Jahn, R.; Francke, U.; Suedhof, T.C.  
J. Biol. Chem. 265, 17267-17273, 1990  
A/Title: Structures and chromosomal localizations of two human genes encoding synaptobrevin  
A/Reference number: A38315; MUID:91009161; PMID:1976629  
A/Accession: B38315  
A/Status: preliminary  
A/Molecule type: DNA  
A/Residues: 1-116 <ARC>  
A/Cross-references: UNIPROT:P19065; GB:M36205; GB:J05611; NID:G338630; PIDN:AAA60604.1; I  
C/Genetics:  
A/Gene: GDB:SYB2; VAMP-2  
A/Cross-references: GDB:125293; OMIM:185861  
A/Map position: 17pter-17p12  
C/Superfamily: synaptobrevin  
C/Keywords: membrane trafficking; transmembrane protein

Query Match 98.3%; Score 170; DB 2; Length 116;  
Best Local Similarity 94.3%; Pred. No. 2.3e-17;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDRADALQAGASXFEKSAKLRKRWKNLK 35  
Db 60 LSELDRADALQAGASXFEKSAKLRKRWKNLK 94

RESULT 2  
UN0011  
synaptobrevin 2 - bovine  
N/Alternate names: SNAP receptor  
C/Species: Bos primigenius taurus (cattle)  
C/Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 09-Jul-2004  
C/Accession: UN0011; S36811; S32363  
R/Suedhof, T.C.; Baumeister, M.; Perin, M.S.; Jahn, R.  
Neuron 2, 1475-1481, 1989  
A/Title: A synaptic vesicle membrane protein is conserved from mammals to Drosophila.  
A/Reference number: A93413; MUID:90180466; PMID:2560644  
A/Accession: UN0011  
A/Molecule type: mRNA  
A/Residues: 1-116 <SUB>  
A/Cross-references: UNIPROT:P19065; GB:X76199; NID:G433075; PIDN:CA451792.1; PID:G433076  
A/Experimental source: brain  
R/Horiikawa, H.P.M.; Saleu, H.; Ichizuka, T.; Sekine, Y.; Tsugita, A.; Odani, S.; Abe, T.  
FEBS Lett. 330, 236-240, 1993  
A/Title: A complex of rab3a, SNAP-25, VAMP/synaptobrevin-2 and syntaxins in brain presyn  
A/Reference number: S36811; MUID:93374072; PMID:8365494  
A/Accession: S36811

A:Molecule type: mRNA  
A:Residues: 'X', 48-79 <HOR>  
A:Experimental source: brain  
R:Soellner, T.; Whiteheart, S.W.; Brunner, M.; Erdjument-Bromage, H.; Geromanos, S.; Temp  
Nature 362, 318-324, 1993  
A:Title: SNAP receptors implicated in vesicle targeting and fusion.  
A:Reference number: S33360; PMID:93205116; PMID:8455717  
A:Accession: S33363  
A:Molecule type: protein  
A:Residues: 31-47, 'X', 49-55, 'X', 57-59; 67-82 <SOE>  
A:Experimental source: brain  
C:Comment: This protein is an intrinsic membrane protein of small synaptic vesicles.  
C:Superfamily: synaptobrevin  
C:Keywords: acetylated amino end; membrane trafficking; transmembrane protein  
F:2-116/Product: synaptobrevin 2 #status predicted <WAT>  
F:95-114/Domain: transmembrane #status predicted <WAT>  
F:2/Modified site: acetylated amino end (Ser) (in mature form) #status predicted

Query Match 98.3%; Score 170; DB 2; Length 116;  
Best Local Similarity 94.3%; Pred. No. 2.3e-17;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASQFESSAAKLKRYWKNLK 35  
60 LSELDDRADALQAGASQFESSAAKLKRYWKNLK 94

RESULT 3  
B34288  
synaptobrevin 2 - rat  
N:Alternate names: vesicle-associated membrane protein 2  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 01-Jun-1990 #sequence\_revision 01-Jun-1990 #text\_change 09-Jul-2004  
C:Accession: B34288; S27125  
R:Ziferink, L.A.; Trimble, W.S.; Scheller, R.H.  
J. Biol. Chem. 264, 11061-11064, 1989  
A:Title: Two vesicle-associated membrane protein genes are differentially expressed in t  
A:Reference number: A34288; PMID:89291844; PMID:2472588  
A:Accession: B34288  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-116 <ZLF>  
A:Cross-references: UNIPROT:Q64357; GB:M24105; GB:U04827; NID:G207626; PIDN:AAA42321.1;  
R:Schlavo, G.; Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; Dasgupta, B.R  
Nature 359, 832-835, 1992  
A:Title: Tetanus and botulinum-B neurotoxins block neurotransmitter release by proteolyt  
A:Reference number: S27125; PMID:93063293; PMID:1331807  
A:Accession: S27125  
A:Molecule type: protein  
A:Residues: 77-99, 'X', 101 <SCH>  
C:Superfamily: synaptobrevin  
C:Keywords: membrane protein; membrane trafficking; synaptic vesicle

Query Match 98.3%; Score 170; DB 2; Length 116;  
Best Local Similarity 94.3%; Pred. No. 2.3e-17;  
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASQFESSAAKLKRYWKNLK 35  
60 LSELDDRADALQAGASQFESSAAKLKRYWKNLK 94

RESULT 4  
S35077  
cellubrevin - rat  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 10-Dec-1993 #sequence\_revision 10-Nov-1995 #text\_change 09-Jul-2004  
C:Accession: S35077  
R:McMahon, H.T.; Uschakov, Y.A.; Edelmann, L.; Link, E.; Binz, T.; Niemann, H.; Jahn, R  
Nature 364, 346-349, 1993  
A:Title: Cellubrevin is a ubiquitous tetanus-toxin substrate homologous to a putative sy  
A:Reference number: S35077; PMID:93333976; PMID:8332193  
A:Accession: S35077

A:Molecule type: mRNA  
A:Residues: 1-103 <MCM>  
A:Cross-references: UNIPROT:Q64271; GB:S63830; NID:G388482; PIDN:AA27554.1; PID:G388483  
C:Superfamily: synaptobrevin

Query Match 95.4%; Score 165; DB 2; Length 103;  
Best Local Similarity 91.4%; Pred. No. 1.1e-16;  
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASQFESSAAKLKRYWKNLK 35  
47 LSELDDRADALQAGASQFESSAAKLKRYWKNLK 81

RESULT 5  
S52747  
Vamp1 protein - human (fragment)  
C:Species: Homo sapiens (man)  
C:Date: 19-May-1995 #sequence\_revision 21-Jul-1995 #text\_change 09-Jul-2004  
C:Accession: S52747  
R:Gough, K.H.; Verkuylen, A.; Cosgrove, L.; Frankel, M.J.; Ward, C.W.  
submitted to the EMBL Data Library, December 1994  
A:Description: Isolation and sequence analysis of SNAREs from human skeletal muscle.  
A:Reference number: S52747  
A:Accession: S52747  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-118 <GOU>  
A:Cross-references: UNIPROT:P23763; EMBL:Z48924; NID:G758107; PIDN:CA88760.1; PID:G75810  
C:Superfamily: synaptobrevin

Query Match 95.4%; Score 165; DB 2; Length 118;  
Best Local Similarity 91.4%; Pred. No. 1.2e-16;  
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASQFESSAAKLKRYWKNLK 35  
62 LSELDDRADALQAGASQFESSAAKLKRYWKNLK 96

RESULT 6  
A38315  
synaptobrevin 1 - human  
C:Species: Homo sapiens (man)  
C:Date: 14-Jun-1991 #sequence\_revision 14-Jun-1991 #text\_change 09-Jul-2004  
C:Accession: A38315  
R:Archer III, B.T.; Oezcelik, T.; Jahn, R.; Francke, U.; Suedhof, T.C.  
U. Biol. Chem. 265, 17267-17273, 1990  
A:Title: Structures and chromosomal localizations of two human genes encoding synaptobrev  
A:Reference number: A38315; PMID:91009161; PMID:1976629  
A:Accession: A38315  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-118 <ARC>  
A:Cross-references: UNIPROT:P23763; GB:M36200; GB:J05611; NID:G338623; PIDN:AAA60603.1; I  
C:Genetics:  
A:Gene: GDB:SYB1; VAMP-1  
A:Cross-references: GDB:125292; OMIM:185880  
A:Map position: 12p-12p  
C:Superfamily: synaptobrevin  
C:Keywords: membrane trafficking; transmembrane protein

Query Match 95.4%; Score 165; DB 2; Length 118;  
Best Local Similarity 91.4%; Pred. No. 1.2e-16;  
Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASQFESSAAKLKRYWKNLK 35  
62 LSELDDRADALQAGASQFESSAAKLKRYWKNLK 96

RESULT 7  
A34288

vesicle-associated membrane protein 1 - rat  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 01-Jun-1990 #sequence\_revision 01-Jun-1990 #text\_change 09-Jul-2004  
 C/Accession: A34288  
 R/RefLink, L.A.; Trimble, W.S.; Scheller, R.H.  
 J. Biol. Chem. 264, 11061-11064, 1999  
 A/Title: Two vesicle-associated membrane protein genes are differentially expressed in  
 A/Reference number: A34288; MUID:89291844; PMID:2472388  
 C/Accession: A34288  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-118 <ELP>  
 A/Cross-references: UNIPROT:Q63666; GB:M24104; GB:J04827; NID:G207628; PIDN:AAA42322.1;  
 C/Superfamily: synaptobrevin  
 C/Keywords: membrane protein

Query Match 95.4%; Score 165; DB 2; Length 118;  
 Best Local Similarity 91.4%; Pred. No. 1.2e-16;  
 Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLRKYWKXK 35  
 |||||  
 DB 62 LSELDDRADALQAGASFEKSAKLRKYWKXK 96

## RESULT 8

A32146  
 vesicle-associated membrane protein 1 - Pacific electric ray  
 C/Species: Torpedo californica (Pacific electric ray)  
 C/Date: 21-May-1990 #sequence\_revision 21-May-1990 #text\_change 09-Jul-2004  
 C/Accession: A32146  
 R/Trimble, W.S.; Cowan, D.M.; Scheller, R.H.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 4538-4542, 1988  
 A/Title: VAMP-1: a synaptic vesicle-associated integral membrane protein.  
 A/Reference number: A32146; MUID:88248054; PMID:3380805  
 A/Accession: A32146  
 A/Molecule type: mRNA  
 A/Residues: 1-120 <TRI>  
 A/Cross-references: UNIPROT:P13701; EMBL:J03777; NID:G213245; PIDN:AAA49286.1; PID:G2132  
 C/Superfamily: synaptobrevin  
 C/Keywords: membrane protein

Query Match 95.4%; Score 165; DB 2; Length 120;  
 Best Local Similarity 91.4%; Pred. No. 1.3e-16;  
 Matches 32; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLRKYWKXK 35  
 |||||  
 DB 64 LSELDDRADALQAGASFEKSAKLRKYWKXK 98

## RESULT 9

S40153  
 synaptobrevin - longfin squid  
 C/Species: Loligo pealeii (longfin squid)  
 C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
 C/Accession: S40153  
 R/Bommerly, K.; Kistner, A.; Haseremann, E.; Betz, H.  
 submitted to the EMBL Data Library, August 1993  
 A/Description: Conservation of primary structure and clostridial neurotoxin cleavage site  
 A/Reference number: S40153  
 A/Accession: S40153  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-125 <BOM>  
 A/Cross-references: UNIPROT:P47194; EMBL:X74748; NID:G437855; PIDN:CAA52766.1; PID:G4378  
 C/Superfamily: synaptobrevin

Query Match 89.6%; Score 155; DB 2; Length 125;  
 Best Local Similarity 82.9%; Pred. No. 3.7e-15;  
 Matches 29; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLRKYWKXK 35

DB 69 LSELDDRADALQAGASQFEKSAKLRKYWKXK 103  
 :|||||

## RESULT 10

T33239  
 synaptobrevin SNB-1 - Caenorhabditis elegans  
 C/Species: Caenorhabditis elegans  
 C/Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
 C/Accession: T33239  
 R/Greco, T.; Bradshaw, H.; O'Brien, D.  
 submitted to the EMBL Data Library, May 1998  
 A/Description: The sequence of C. elegans cosmid T10H9.  
 A/Reference number: T33239  
 A/Accession: T33239  
 A/Status: preliminary; translated from GB/EMBL/DD3U  
 A/Molecule type: DNA  
 A/Residues: 1-109 <GRE>

A/Cross-references: UNIPROT:O02495; EMBL:AF067949; PIDN:AA019234.1; GSPDB:GN00023; CESP:1  
 A/Experimental source: strain Bristol N2; clone T10H9  
 A/Genetics: C/Genetics: SNB-1; CESP:T10H9.4  
 A/Map position: 5  
 A/Introns: 39/3  
 C/Superfamily: synaptobrevin

Query Match 88.4%; Score 153; DB 2; Length 109;  
 Best Local Similarity 82.9%; Pred. No. 6.3e-15;  
 Matches 29; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLRKYWKXK 35  
 |||||  
 DB 52 LSELDDRADALQAGASQFEKSAKLRKYWKXK 86

## RESULT 11

S35555  
 vesicle-associated membrane protein 2 - chicken (fragment)  
 C/Species: Gallus gallus (chicken)  
 C/Date: 10-Dec-1993 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004  
 C/Accession: S35555  
 R/Paternello, T.; Bargelloni, L.; Rossetto, O.; Schiavo, G.; Montecucco, C.  
 Nature 364, 581-582, 1993  
 A/Title: Neurotransmission and secretion.  
 A/Reference number: S35552; MUID:93354436; PMID:8350916  
 A/Accession: S35555  
 A/Molecule type: DNA  
 A/Residues: 1-32 <PAT>  
 A/Cross-references: UNIPROT:O7L264  
 C/Superfamily: synaptobrevin  
 C/Keywords: membrane trafficking; transmembrane protein

Query Match 67.1%; Score 116; DB 2; Length 32;  
 Best Local Similarity 92.6%; Pred. No. 3.9e-10;  
 Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXFEKSAKLR 27  
 |||||  
 DB 6 LSELDDRADALQAGASQFEKSAKLR 32

## RESULT 12

S35553  
 vesicle-associated membrane protein 1 - chicken (fragment)  
 C/Species: Gallus gallus (chicken)  
 C/Date: 20-May-1994 #sequence\_revision 13-Mar-1997 #text\_change 09-Jul-2004  
 C/Accession: S35553  
 R/Paternello, T.; Bargelloni, L.; Rossetto, O.; Schiavo, G.; Montecucco, C.  
 Nature 364, 581-582, 1993  
 A/Title: Neurotransmission and secretion.  
 A/Reference number: S35552; MUID:93354436; PMID:8350916  
 A/Accession: S35553  
 A/Molecule type: DNA

A;Residues: 1-32 <PAT>  
A;Cross-references: UNIPROT:Q7LZ65  
C;Superfamily: synaptoobrevin

Query Match 67.1%; Score 116; DB 2; Length 32;  
Best Local Similarity 92.6%; Pred. No. 3.9e-10;  
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDRADALQAGSXFEXSAKLKR 27  
DB 6 LSELDRADALQAGSXFESSAKLKR 32

## RESULT 13

S35554  
vesicle-associated membrane protein 2 - mouse (fragment)

C;Species: Mus musculus (house mouse)  
C;Date: 10-Dec-1993 #sequence\_revision 27-Feb-1997 #text\_change 09-Jul-2004  
C;Accession: S35554  
R;Paternello, T.; Bargelloni, L.; Rossetto, O.; Schiavo, G.; Montecucco, C.  
Nature 364, 581-582, 1993

A;Title: Neurotransmission and secretion.  
A;Reference number: S35552; MUID:93354436; PMID:8350916  
A;Accession: S35554

A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-32 <PAT>  
A;Cross-references: UNIPROT:Q35619  
C;Superfamily: synaptoobrevin

Query Match 67.1%; Score 116; DB 2; Length 32;  
Best Local Similarity 92.6%; Pred. No. 3.9e-10;  
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDRADALQAGSXFEXSAKLKR 27  
DB 6 LSELDRADALQAGSXFESSAKLKR 32

## RESULT 14

S35552  
vesicle-associated membrane protein 1 - mouse (fragment)

C;Species: Mus musculus (house mouse)  
C;Date: 10-Dec-1993 #sequence\_revision 27-Feb-1997 #text\_change 09-Jul-2004  
C;Accession: S35552  
R;Paternello, T.; Bargelloni, L.; Rossetto, O.; Schiavo, G.; Montecucco, C.  
Nature 364, 581-582, 1993

A;Title: Neurotransmission and secretion.  
A;Reference number: S35552; MUID:93354436; PMID:8350916  
A;Accession: S35552

A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-32 <PAT>  
A;Cross-references: UNIPROT:Q9CXX2  
C;Superfamily: synaptoobrevin

Query Match 67.1%; Score 116; DB 2; Length 32;  
Best Local Similarity 92.6%; Pred. No. 3.9e-10;  
Matches 25; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDRADALQAGSXFEXSAKLKR 27  
DB 6 LSELDRADALQAGSXFESSAKLKR 32

## RESULT 15

JC1522  
synaptoobrevin isoform B - fruit fly (Drosophila melanogaster)

N;Alternate names: vesicle-associated membrane protein B  
C;Species: Drosophila melanogaster  
C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 09-Jul-2004  
C;Accession: JC1522  
R;Chen, A.C.; Burgess, R.W.; Wong, B.R.; Schwarz, T.L.; Scheller, R.H.

Gene 131, 175-181, 1993  
A;Title: Differential expression of transcripts from syb, a Drosophila melanogaster gene  
A;Reference number: JC1521; MUID:94010306; PMID:8406010

A;Accession: JC1522  
A;Molecule type: DNA  
A;Residues: 1-132 <CHI>  
A;Cross-references: UNIPROT:P18489; GB:U14270; NID:9290281; PIDN:AAA28923.1; PID:9290282  
A;Note: the authors translated the codon AAG for residue 101 as Asn and CGC for residue 1

C;Comment: Gene syb comprises five exons. Splicing exons 1.2.3.4.5 results in synaptoobrevin  
C;Genetics:  
A;Gene: syb  
A;Cross-references: FlyBase:FBgn0003660  
A;Introns: 16/2; 128/1  
C;Superfamily: synaptoobrevin

C;Keywords: membrane protein; synaptic vesicle

Query Match 65.3%; Score 113; DB 2; Length 132;  
Best Local Similarity 62.9%; Pred. No. 4.7e-09;  
Matches 22; Conservative 3; Mismatches 10; Indels 0; Gaps 0;

QY 1 LSELDRADALQAGSXFEXSAKLKRKYWKULK 35  
DB 76 LSELGERADQLFGAGSGSEQAGKLRKQKWMNMK 110

Search completed: November 1, 2004, 17:53:52  
Job time : 19.125 secs





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OX  NCBI_TaxID=8364;
RN  [1]
RN  SEQUENCE FROM N.A.
RC  MEDLINE=22388257; PubMed=12477932;
RX  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA  Krausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA  Altschuler S.F., Zeeberg B., Buettow K., Schaefer C.F., Bhat N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Stapleton M., Soares M.B., Donald W.F., Casavant T.L., Scheetz T.E.,
RA  Brownstein M.J., Ustin T.B., Toshitsuki S., Carninci P., Prange C.,
RA  Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA  Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA  Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA  Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA  Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA  Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA  Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA  Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA  Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA  Krzywiński M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA  Jones S.J., Marra M.A.;
RT  "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RN  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN  SEQUENCE FROM N.A.
RC  TISSUE=Embryo;
RA  Klein S., Strausberg R.;
RX  Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR  EMBL: BC061396; AAH61396.1; -
DR  InterPro: IPR001388; Synapcobrevin.
DR  Pfam: PF00957; Synapcobrevin; 1.
DR  PRINTS: PR00219; SYNAPCOTREVIN.
DR  PRODOM: PD001229; Synapcobrevin; 1.
DR  PROSITE: PS00417; SYNAPCOTREVIN; 1.
DR  PROSITE: PS00892; V SNARE; 1.
DR  Hypothetical protein;
SQ  SEQUENCE 114 AA; 12440 MW; 0EE3EADBDP2A1ABE CRC64;

Query Match 98.3%; Score 170; DB 2; Length 114;
Best Local Similarity 94.3%; Pred. No. 8.8e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  1 LSELDPRADALQAGASQFETSAKLRKRYWKNLK 35
Db 58 LSELDPRADALQAGASQFETSAKLRKRYWKNLK 92

RESULT 3
AAH61396 PRELIMINARY; PRT; 114 AA.
AC  AAH61396;
DT  25-MAR-2004 (TrEMBLrel. 27, Created)
DT  25-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT  25-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE  Hypothetical protein MGC75977.
GN  MGC75977.
OS  Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
OC  Xenopodinae; Xenopus; Silurana.
NCBI_TaxID=8364;
[1]
RN  SEQUENCE FROM N.A.
RC  TISSUE=Embryo;
RX  MEDLINE=22388257; PubMed=12477932;
RA  Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA  Krausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA  Altschuler S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
RA  Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA  Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA  Stapleton M., Soares M.B., Donald W.F., Casavant T.L., Scheetz T.E.,

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RA  Brownstein M.J., Ustin T.B., Toshitsuki S., Carninci P., Prange C.,
RA  Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA  Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA  Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W.,
RA  Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA  Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA  Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA  Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA  Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA  Krzywiński M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA  Jones S.J., Marra M.A.;
RT  "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RN  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN  SEQUENCE FROM N.A.
RC  TISSUE=Embryo;
RA  Klein S., Strausberg R.;
RX  Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR  EMBL: BC061396; AAH61396.1; -
DR  Hypothetical protein.
SQ  SEQUENCE 114 AA; 12440 MW; 0EE3EADBDP2A1ABE CRC64;

Query Match 98.3%; Score 170; DB 2; Length 114;
Best Local Similarity 94.3%; Pred. No. 8.8e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY  1 LSELDPRADALQAGASQFETSAKLRKRYWKNLK 35
Db 58 LSELDPRADALQAGASQFETSAKLRKRYWKNLK 92

RESULT 4
VAM2 HUMAN STANDARD; PRT; 115 AA.
AC  P19065;
DT  01-NOV-1990 (Rel. 16, Created)
DT  01-NOV-1997 (Rel. 35, Last sequence update)
DT  01-OCT-2004 (Rel. 45, Last annotation update)
DE  Vesicle-associated membrane protein 2 (VAMP-2) (Synapcobrevin 2).
GN  Name=VAMP2; Synonyms=SYB2;
OS  Homo sapiens (Human), and
OS  Bos taurus (Bovine).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606; 9913;
[1]
RN  SEQUENCE FROM N.A.
RC  SPECIES=Human;
RX  MEDLINE=9100916; PubMed=1976629;
RA  Archer B.T. III, Oezcelik T., Jahn R., Franke U., Suedhof T.C.;
RT  "Structures and chromosomal localizations of two human genes encoding
synapcobrevin 1 and 2."
RL  J. Biol. Chem. 265:17267-17273(1990).
[2]
RN  SEQUENCE FROM N.A.
RC  SPECIES=Human; TISSUE=Peripheral blood;
RA  Nabokina S.M., Lazo P.A., Molinero F.;
RT  "Expression of VAMP genes in human neutrophils.";
RL  Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
[3]
RN  SEQUENCE FROM N.A.
RC  SPECIES=Human; TISSUE=Blood;
RA  Tarusio D., Zorag K.G., Falbo V.;
RT  "Genomic structure of human SYB2 gene."
RL  Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
[4]
RN  SEQUENCE FROM N.A.
RC  SPECIES=Bovine;
RX  MEDLINE=90180466; PubMed=2560644;
RA  Suedhof T.C., Baumeister M., Perin M.S., Jahn R.;
RT  "A synaptic vesicle membrane protein is conserved from mammals to
Drosophila."

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RN Neuron 2:1475-1481(1989).  
 RN [5]  
 RP SEQUENCE OF 31-59 AND 67-82, AND ACETYLATION.  
 RC SPECIES=Bovine;  
 RX MEDLINE=93205116; PubMed=8455717;  
 RA Scollner T., Whiteheart S.W., Brunner M., Erdjument-Bromage H.,  
 RA Germaines S., Tempst P., Rothman J.E.,  
 RT "SNAP receptors implicated in vesicle targeting and fusion.",  
 RT Nature 362:318-324(1993).  
 RN [6]  
 RP TISSUE SPECIFICITY.  
 RC SPECIES=Human;  
 RX MEDLINE=96332494; PubMed=8760387;  
 RA Jagadeesh M.N., Fernandez C.S., Hewish D.R., Macaulay S.L., Gough K.H.,  
 RA Grusovin J., Verkhran A., Cosgrove L., Alfacci A., Frenkel M.J.,  
 RA Ward C.W.;  
 RT "Insulin-responsive tissues contain the core complex protein SNAP-25  
 (synaptosomal-associated protein 25) A and B isoforms in addition to  
 RT syntaxin 4 and synaptobrevins 1 and 2.",  
 RT Biochem. J. 317:945-954(1996).  
 RN [7]  
 RP TOPOLOGY.  
 RC SPECIES=Human;  
 RX MEDLINE=95137000; PubMed=7835332;  
 RA Kutay U., Ahnert-Hilger G., Hartmann E., Wiedenmann B., Rapoport T.A.,  
 RT "Transport route for synaptobrevin via a novel pathway of insertion  
 RT into the endoplasmic reticulum membrane.",  
 RT EMBO J. 14:217-223(1995).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 33-88 IN COMPLEX WITH BOTB.  
 RC SPECIES=Human;  
 RX MEDLINE=20392548; PubMed=10932255; DOI=10.1038/77997;  
 RA Hanson M.A., Stevens R.C.;  
 RT "Cocrystal structure of synaptobrevin-II bound to botulinum neurotoxin  
 RT type B at 2.0 A resolution",  
 RT Nat. Struct. Biol. 7:687-692(2000).  
 CC -1- FUNCTION: Involved in the targeting and/or fusion of transport  
 CC vesicles to their target membrane.  
 CC -1- SUBUNIT: Interacts with VAMP and VAMPB.  
 CC -1- SUBCELLULAR LOCATION: Type IV membrane protein. Neuronal synaptic  
 CC vesicles.  
 CC -1- TISSUE SPECIFICITY: Nervous system and skeletal muscle.  
 CC -1- SIMILARITY: Belongs to the synaptobrevin family.  
 CC -1- SIMILARITY: Contains 1 v-SNARE coiled-coil homology domain.  
 CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 DR EMBL: M36205; AAA60604.1; -  
 DR EMBL: M36201; AAA60604.1; JOINED.  
 DR EMBL: M36202; AAA60604.1; JOINED.  
 DR EMBL: M36203; AAA60604.1; JOINED.  
 DR EMBL: M36204; AAA60604.1; JOINED.  
 DR EMBL: AJ225044; CA112385.1; -  
 DR EMBL: AF135372; AAF15551.1; -  
 DR EMBL: X76199; CA53792.1; -  
 DR PIR: B38315; B38315.  
 DR PIR: JN0011; JN0011.  
 DR PDB: 1P83; X-ray; B=52-75, C=76-87.  
 DR GeneW; HGNC:12643; VAMP2.  
 DR MIM; 185881; -  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR InterPro; IPR001388; Synaptobrevin.  
 DR Pfam; PF00957; Synaptobrevin; 1.  
 DR PRINTS; PR00219; SYNAPTOBREVN.  
 DR ProDom; PD001229; Synaptobrevin; 1.  
 DR PROSITE; PS00417; SYNAPTOBREVN; 1.  
 DR PROSITE; PS00892; V-SNARE; 1.

KW 3D-structure; Acetylation; Coiled coil; Direct protein sequencing;  
 KM Multigene family; Synapse; Synaptosome; Transmembrane.  
 FT INIT MET 0 0  
 FT DOMAIN 1 93 Cytoplasmic (Potential).  
 FT TRANSMEM 94 113 Anchor for type IV membrane protein  
 FT 113 (Potential).  
 FT DOMAIN 114 115 Vesicular (Potential).  
 FT MOD\_RES 1 1 N-acetylserine.  
 FT DOMAIN 30 90 v-SNARE coiled-coil homology.  
 FT SEQUENCE 115 AA; 12517 MW; 388B79F0D21AD81E CRC64;  
 SQ  
 Query Match 98.3%; Score 170; DB 1; Length 115;  
 Best Local Similarity 94.3%; Pred. No. 8.9e-17;  
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 DB 1 LSELDPRADALQAGASXFEKSAKTKRKYWKXNK 35  
 59 LSELDPRADALQAGASOFETSAKTKRKYWKXNK 93  
 RESULT 5  
 VAMP2 MOUSE STANDARD; PRT; 115 AA.  
 ID VAMP2 MOUSE  
 AC 064357;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-OCT-2004 (Rel. 45, Last annotation update)  
 DE Vesicle-associated membrane protein 2 (VAMP-2) (Synaptobrevin 2).  
 GN Name=Vamp2; Synonyms=Synd2;  
 OS Mus musculus (Mouse);  
 OS Rattus norvegicus (Rat);  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090, 10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Rat;  
 RX MEDLINE=89291844; PubMed=2472388;  
 RA Eiferink L.A., Trimble W.S., Scheieler R.H.;  
 RT "Two vesicle-associated membrane protein genes are differentially  
 RT expressed in the rat central nervous system.",  
 RT J. Biol. Chem. 264:11061-11064(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC SPECIES=Mouse;  
 RX MEDLINE=98104125; PubMed=9430681;  
 RA Martin L.B., Shewan A., Millar C.A., Gould G.W., James D.E.;  
 RT "Vesicle-associated membrane protein 2 plays a specific role in the  
 RT insulin-dependent trafficking of the facilitative glucose transporter  
 RT GLUT4 in 3T3-L1 adipocytes.",  
 RT J. Biol. Chem. 273:1444-1452(1998).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 1-96 IN COMPLEX WITH STX1A  
 RP AND SNAP25.  
 RC SPECIES=Rat;  
 RX MEDLINE=98450524; PubMed=9759724; DOI=10.1038/26412;  
 RA Sutton R.B., Fasshauer D., Jahn R., Brunger A.T.;  
 RT "Crystal structure of a SNARE complex involved in synaptic exocytosis  
 RT at 2.4 A resolution.",  
 RT Nature 395:347-353(1998).  
 RN [4]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 28-93 IN COMPLEX WITH STX1A;  
 RP CEX1 AND SNAP25, AND NMR ANALYSIS.  
 RC SPECIES=Rat;  
 RX MEDLINE=21822661; PubMed=11832227;  
 RA Chen X., Tomchick D.R., Kovrigin E., Arac D., Machius M.,  
 RA Suedhof T.C., Rizo J.;  
 RT "Three-dimensional structure of the complexin/SNARE complex.",  
 RT Neuron 33:397-409(2002).  
 RN [5]  
 RP X-RAY CRYSTALLOGRAPHY (1.45 ANGSTROMS) OF 28-89 IN COMPLEX WITH STX1A  
 RP AND SNAP25.  
 RC SPECIES=Rat;

RA MEDLINE=2249607; PubMed=12496247; DOI=10.1074/jbc.M211869200;  
 RA Ernst J.A., Brunger A.T.;  
 RT "High resolution structure, stability, and synaptobrevin binding of a  
 RT truncated neuronal SNARE complex.";  
 RL J. Biol. Chem. 278:8630-8636(2003).  
 CC -1- FUNCTION: Involved in the targeting and/or fusion of transport  
 CC vesicles to their target membrane.  
 CC -1- SUBUNIT: Interacts with VAMP and VAPB (by similarity). Part of the  
 CC SNARE core complex containing SNAP25, VAMP2 and syntaxin. This  
 CC complex binds to CPLX1.  
 CC -1- SUBCELLULAR LOCATION: Type IV membrane protein. Neuronal synaptic  
 CC vesicles.  
 CC -1- TISSUE SPECIFICITY: Nervous system specific. A higher level  
 CC expression is seen in the brain as compared to the spinal cord.  
 CC -1- SIMILARITY: Belongs to the synaptobrevin family.  
 CC -1- SIMILARITY: Contains 1 V-SNARE coiled-coil homology domain.  
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; M24105; AAA42321.1; -  
 DR EMBL; U60150; AAB03463.1; -  
 DR PIR; B34288; B34288.  
 DR PDB; 1K1T; X-ray; A=26-91.  
 DR PDB; 1N7S; X-ray; A=26-88.  
 DR PDB; 1SFC; X-ray; A/E/I=1-95.  
 DR WGI; MGI:1313277; Vamp2.  
 DR RGD; 3949; Vamp2.  
 DR InterPro; IPR001388; Synaptobrevin.  
 DR Pfam; PF00957; Synaptobrevin.  
 DR PRINTS; PR00219; SYNAPTOBREVN.  
 DR ProDom; PD001229; SYNAPTOBREVN.  
 DR PROSITE; PS00417; SYNAPTOBREVN; 1.  
 DR PROSITE; PS00957; SYNAPTOBREVN; 1.  
 DR PROSITE; PS00952; V-SNARE; 1.  
 DR 3D-structure; Acetylation; Coiled coil; Multigene family;  
 DR Polymorphism; Synapse; Synaptosome; Transmembrane.  
 DR INIT MET 0  
 FT DOMAIN 1 93 By similarity.  
 FT TRANSMEM 94 113 Cytoplasmic (Potential).  
 FT 114 115 Anchor for type IV membrane protein  
 FT 114 115 Vesicular (Potential).  
 FT MOD RES 1 1 N-acetylserine (by similarity).  
 FT DOMAIN 30 90 V-SNARE coiled-coil homology.  
 FT VARIANT 110 110 I -> I.  
 FT VARIANT 111 111 V -> I.  
 FT HELIX 28 87  
 SQ SEQUENCE 115 AA; 12559 MW; EA40D6291ABF0BC CRC64;  
 Query Match 98.3%; Score 170; DB 1; Length 115;  
 Best Local Similarity 94.3%; Pred. No. 8, 9e-17;  
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 LSELDDRADALQAGASXFEKSAKLRKYWKXNLK 35  
 Db 59 LSELDDRADALQAGASQFETSAKLRKYWKXNLK 93  
 RESULT 6  
 ID Q9BUC2 PRELIMINARY; PRT; 116 AA.  
 AC Q9BUC2;  
 DT 01-JUN-2001 (Tremblrel. 17, Created)  
 DT 01-JUN-2001 (Tremblrel. 17, Last sequence update)  
 DT 01-OCT-2004 (Tremblrel. 28, Last annotation update)  
 DE Vesicle-associated membrane protein 2 (Synaptobrevin 2).  
 GN Name:VAMP2;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Euthera; Primates; Catarrhini; Homiidae; Homo.  
 OC NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain, Lung, and Testis;  
 RX MEDLINE=2238257; PubMed=12477932;  
 RA Strausberg R.B., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,  
 RA Datchenko L., Marmura K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.O., Usdin T.B., Toshiyuki S., Carninci P., Pange C.,  
 RA Rana S.S., Loughran N.A., Peters G.J., Abramson C.D., Mullaney S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.O., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalón D.K., Mazny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Vahedi J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Kravinsky W.I., Skalska U., Smalton D.B., Schnerch A., Schein U.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Strausberg R.;  
 RN Submitted (Feb-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RA Strausberg R.;  
 RN Submitted (Dec-2001) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RA Strausberg R.;  
 RN Submitted (Jul-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC002737; AAH02737.3; -  
 DR EMBL; BC019608; AAH19608.1; -  
 DR EMBL; BC033870; AAH33870.1; -  
 DR HSR; Q9WUW2; 1SFC.  
 DR InterPro; IPR001388; Synaptobrevin.  
 DR Pfam; PF00957; Synaptobrevin; 1.  
 DR PRINTS; PR00219; SYNAPTOBREVN.  
 DR ProDom; PD001229; SYNAPTOBREVN; 1.  
 DR PROSITE; PS00417; SYNAPTOBREVN; 1.  
 DR PROSITE; PS00952; V-SNARE; 1.  
 SQ SEQUENCE 116 AA; 12663 MW; 9CDD679C4F6F1B5A8 CRC64;  
 Query Match 98.3%; Score 170; DB 2; Length 116;  
 Best Local Similarity 94.3%; Pred. No. 9e-17;  
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 1 LSELDDRADALQAGASXFEKSAKLRKYWKXNLK 35  
 Db 60 LSELDDRADALQAGASQFETSAKLRKYWKXNLK 94  
 RESULT 7  
 ID Q9NOY0 PRELIMINARY; PRT; 116 AA.  
 AC Q9NOY0;  
 DT 01-OCT-2000 (Tremblrel. 15, Created)  
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)  
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
 DE VAMP-2.  
 GN Macaca mulatta (Rhesus macaque).  
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Euthera; Primates; Catarrhini; Cercopithecoidea;

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OC Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISUS=Hippocampus;
RA Jensen M.J., Smith L.A.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF240769; AAF64476.1; -.
DR HSSP; Q9WUW2; ISPC.
DR InterPro; IPR001388; Synaptoobrevin.
DR Pfam; PF00857; Synaptoobrevin.1.
DR PRINTS; PR00219; SYNAPTOBREVN.
DR PRODOM; PD001229; SYNAPTOBREVN.1.
DR PROSITE; PS00417; SYNAPTOBREVN.1.
DR PROSITE; PS50892; V_SNARE.1.
SQ SEQUENCE 116 AA; 12663 MW; 9CD679C4F6F1B5A8 CRC64;

Query Match 98.3%; Score 170; DB 2; Length 116;
Best Local Similarity 94.3%; Pred. No. 9e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LSELDPRADALQAGASXFEKSAKLRKRYWKNLK 35
DB 60 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 94

RESULT 8
OY 035619 PRELIMINARY; PRT; 116 AA.
ID 035619;
AC 035619;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-JAN-2004 (TREMBLrel. 26, Last annotation update)
DE Vesicle associated membrane protein 2.
GN Name=Vamp2; Synonyms=vamp-2;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Olsen S.K., Doerre S., Corley R.B.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF007168; AAB62931.1; -.
DR PIR; S35554; S35554.
DR HSSP; Q9WUW2; ISPC.
DR MGD; MGI:1313277; Vamp2.
DR GO; GO:0030141; C:secretory granule; IDA.
DR GO; GO:0030672; C:synaptic vesicle membrane; IDA.
DR GO; GO:0042589; C:cytosol granule membrane; IDA.
DR GO; GO:0005516; F:calmodulin binding; IDA.
DR GO; GO:0005543; F:phospholipid binding; IDA.
DR GO; GO:000143; F:SNARE binding; IDA.
DR GO; GO:001156; P:calcium ion-dependent exocytosis; IDA.
DR GO; GO:001157; P:regulation of exocytosis; IDA.
DR GO; GO:0016083; P:synaptic vesicle fusion; IMP.
DR InterPro; IPR001388; Synaptoobrevin.
DR Pfam; PF00957; Synaptoobrevin.1.
DR PRINTS; PR00219; SYNAPTOBREVN.
DR PRODOM; PD001229; SYNAPTOBREVN.1.
DR PROSITE; PS00417; SYNAPTOBREVN.1.
DR PROSITE; PS50892; V_SNARE.1.
SQ SEQUENCE 116 AA; 12677 MW; 4E1D0D56B5409D0A CRC64;

Query Match 98.3%; Score 170; DB 2; Length 116;
Best Local Similarity 94.3%; Pred. No. 9e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LSELDPRADALQAGASXFEKSAKLRKRYWKNLK 35
DB 60 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 94

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RESULT 9
AAH02737 PRELIMINARY; PRT; 116 AA.
AC AAH02737;
DT 14-APR-2004 (TREMBLrel. 27, Created)
DT 14-APR-2004 (TREMBLrel. 27, Last sequence update)
DT 14-APR-2004 (TREMBLrel. 27, Last annotation update)
DE Vesicle-associated membrane protein 2 (Synaptoobrevin 2).
GN VAMP2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISUS=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Uedini T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mallary S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Koriy K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.O., Maira M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISUS=Brain;
RA Strausberg R.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC002737; AAH02737.3; -.
SQ SEQUENCE 116 AA; 12663 MW; 9CD679C4F6F1B5A8 CRC64;

Query Match 98.3%; Score 170; DB 2; Length 116;
Best Local Similarity 94.3%; Pred. No. 9e-17;
Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LSELDPRADALQAGASXFEKSAKLRKRYWKNLK 35
DB 60 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 94

RESULT 10
AAH5105 PRELIMINARY; PRT; 116 AA.
AC AAH5105;
DT 14-APR-2004 (TREMBLrel. 27, Created)
DT 14-APR-2004 (TREMBLrel. 27, Last sequence update)
DT 14-APR-2004 (TREMBLrel. 27, Last annotation update)
DE Vesicle-associated membrane protein 2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISUS=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

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RA Hopkings R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Schetz T.E.,  
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loggiano N.A., Peters G.J., Abirson R.D., Mullighan S.J.,  
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalón D.K., Murthy D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Faney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Butterfield Y.S.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzyzanski M.I., Skalska U., Smalish D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Strausberg R.;  
 RT Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL, BC055105; AHS5105.1; -; 4A0DD56B5409D0A CRC64;  
 SQ SEQUENCE 116 AA; 12691 MW; 4A0DD56B5409D0A CRC64;  
 Query Match 98.3%; Score 170; DB 2; Length 116;  
 Best Local Similarity 94.3%; Pred. No. 9e-17;  
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Oy 1 LSELDPRADALQAGASFEKSAKLRKRYWKXK 35  
 Db 60 LSELDPRADALQAGASFEKSAKLRKRYWKXK 94  
 RESULT 11  
 ID BAC41125 PRELIMINARY; PRT; 116 AA.  
 AC BAC41125;  
 DT 14-APR-2004 (Tremblrel. 27, Created)  
 DT 14-APR-2004 (Tremblrel. 27, Last sequence update)  
 DT 14-APR-2004 (Tremblrel. 27, Last annotation update)  
 DE 15 days embryo brain cDNA, RIKEN full-length enriched library,  
 DE clone/G60012G02 product:unclassified, full insert sequence.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Brain;  
 RX MEDLINE=22354683; PubMed=12466851;  
 RA The FANTOM Consortium,  
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs";  
 RL Nature 420:563-573(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Brain;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection";  
 RL Nature 409:685-690(2001).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Brain;  
 RX MEDLINE=99279253; PubMed=10349636;  
 RA Carninci P., Hayashizaki Y.,  
 RT "High-efficiency full-length cDNA cloning";  
 RL Mech. Enzymol. 303:19-44(1999).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Brain;

RX MEDLINE=20499374; PubMed=11042159;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes";  
 RL Genome Res. 10:1617-1630(2000).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Brain;  
 RX MEDLINE=20530913; PubMed=11076861;  
 RA Shibata K., Itoh M., Aizawa K., Nagao S., Sasaki N., Carninci P.,  
 RA Kono H., Akiyama U., Nishi K., Kikunai T., Tashiro H., Itoh M.,  
 RA Suni N., Ishii Y., Nakamura S., Hazama M., Nishino T., Harada A.,  
 RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Obara E., Watabiki M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsuzaki S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kita A., Hayashizaki Y.;  
 RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer";  
 RL Genome Res. 10:1757-1771(2000).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Brain;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,  
 RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Hori F., Imocani K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,  
 RA Katoh H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,  
 RA Kurihara K., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohata N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toya T., Yasunishi A., Muramatsu M., Hayashizaki Y.;  
 RT Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 RL EMBL, AK090178; BAC41125.1; -;  
 DR EMBL, AK090178; BAC41125.1; -;  
 SQ SEQUENCE 116 AA; 12691 MW; 4A0DD56B5409D0A CRC64;  
 Query Match 98.3%; Score 170; DB 2; Length 116;  
 Best Local Similarity 94.3%; Pred. No. 9e-17;  
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 Oy 1 LSELDPRADALQAGASFEKSAKLRKRYWKXK 35  
 Db 60 LSELDPRADALQAGASFEKSAKLRKRYWKXK 94  
 RESULT 12  
 ID Q9WUM2 PRELIMINARY; PRT; 135 AA.  
 AC Q9WUM2;  
 DT 01-NOV-1999 (Tremblrel. 12, Created)  
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)  
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)  
 DE Vesicle associated membrane protein 2B.  
 GN Name=vamp2;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RX MEDLINE=99297576; PubMed=10371166;  
 RA Mandic R., Lowe A.W.;  
 RT "Characterization of an alternatively spliced isoform of rat vesicle  
 RT associated membrane protein-2 (VAMP-2).";  
 RL FEBS Lett. 451:209-213(1999).  
 DR EMBL, AJ131104; CAB43509.1; -;  
 DR InterPro; IPR001388; SynapcObrevin; 1.  
 DR Pfam; PF00957; SynapcObrevin; 1.  
 DR PRINTS; PR00219; SynapcObrevin; 1.  
 DR ProDom; PD001229; SynapcObrevin; 1.

DR PROSITE, PS00417; SYNAPTOBREVIN; 1.  
 DR PROSITE, PS50892; V\_SNAKE; 1.  
 SQ SEQUENCE 135 AA; 14509 MW; F37D14A87BDAB1FE CRC64;  
 Query Match 98.3%; Score 170; DB 2; Length 135;  
 Best Local Similarity 94.3%; Pred. No. 1,1e-16;  
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LSELDDRADALQAGASXFEKSAKLRKRYWKNLK 35  
 |||  
 DB 60 LSELDDRADALQAGASQFETSAAKLRKRYWKNLK 94  
 |||

RESULT 13  
 ID Q8CHRA PRELIMINARY; PRT; 142 AA.  
 AC Q8CHRA;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Vamp2 protein (Fragment).  
 OS Name=Vamp2;  
 GN Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
 RX MEDLINE=22388257; PubMed=1247932;  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Dichtenko L., Marusha K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stopleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carrinci P., Prange C.,  
 RA Raza S.S., Loquellano N.A., Peters G.J., Adamson R.D., Mullady S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Paley J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,  
 RA Krzywinski M.I., Skalske U., Smalins D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Maitz M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
 RA Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL, BC039745; AA039745.1; -.  
 DR HSSP; Q9KWM2; ISFC.  
 DR MGD; MGI:131377; Vamp2.  
 DR GO; GO:0030141; C:secretory granule; IDA.  
 DR GO; GO:0030672; C:synaptic vesicle membrane; IDA.  
 DR GO; GO:0042589; C:zymogen granule membrane; IDA.  
 DR GO; GO:0005516; F:calmodulin binding; IDA.  
 DR GO; GO:0005343; F:phospholipid binding; IDA.  
 DR GO; GO:0000149; F:SNARE binding; IDA.  
 DR GO; GO:0071156; P:calcium ion-dependent exocytosis; IDA.  
 DR GO; GO:0071157; P:regulation of exocytosis; IDA.  
 DR GO; GO:0016083; P:synaptic vesicle fusion; IMP.  
 DR InterPro: IPR001388; SynaptoBrevin.  
 DR Pfam: PF00957; SynaptoBrevin.1.  
 DR PRINTS; PR00219; SYNAPTOBREVN.  
 DR ProDom; PD001229; SYNAPTOBREVN.  
 DR PROSITE, PS00417; SYNAPTOBREVIN; 1.  
 DR PROSITE, PS50892; V\_SNAKE; 1.

FT NON\_TER 1 1  
 SQ SEQUENCE 142 AA; 15313 MW; F1B0C9C93A95B776 CRC64;  
 Query Match 98.3%; Score 170; DB 2; Length 142;  
 Best Local Similarity 94.3%; Pred. No. 1,1e-16;  
 Matches 33; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LSELDDRADALQAGASXFEKSAKLRKRYWKNLK 35  
 |||  
 DB 86 LSELDDRADALQAGASQFETSAAKLRKRYWKNLK 120  
 |||

RESULT 14  
 ID VAMP2\_XENLA STANDARD; PRT; 113 AA.  
 AC P47193;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 15-DEC-1998 (Rel. 37, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Vesicle-associated membrane protein 2 (VAMP-2) (SynaptoBrevin 2)  
 DE (SYBIT).  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OX Xenopodidae; Xenopus.  
 OX NCBI\_TaxId=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wang X.-H., Poo M.-M.;  
 RA Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 32-113 FROM N.A.  
 RC TISSUE=Embryo;  
 RX MEDLINE=95324415; PubMed=7601005;  
 RA Knecht A.K., Good P.U., David J.B., Harland R.M.;  
 RT "Dorsal-ventral patterning and differentiation of noggin-induced  
 neural tissue in the absence of mesoderm";  
 RL Development 121:1927-1935(1995).  
 CC -1- FUNCTION: Involved in the targeting and/or fusion of transport  
 vesicles to their target membrane.  
 CC -1- SUBCELLULAR LOCATION: Type IV membrane protein. Neuronal synaptic  
 vesicles.  
 CC -1- SIMILARITY: Belongs to the synaptoBrevin family.  
 CC -1- SIMILARITY: Contains 1 V-SNARE coiled-coil homology domain.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL, AF035017; AA088138.1; -.  
 DR EMBL, U16801; AA01376.1; -.  
 DR HSSP; P19065; IPR3.  
 DR InterPro: IPR001388; SynaptoBrevin.  
 DR Pfam; PF00957; SynaptoBrevin.1.  
 DR PRINTS; PR00219; SYNAPTOBREVN.  
 DR ProDom; PD001229; SYNAPTOBREVN.  
 DR PROSITE, PS00417; SYNAPTOBREVIN; 1.  
 DR PROSITE, PS50892; V\_SNAKE; 1.  
 DR Acetylation; Coiled coil; Multigene family; Synapse; Synaposome;  
 KW Transmembrane.  
 FT INIT MET 0  
 FT DOMAIN 1 91 By similarity.  
 FT TRANSMEM 92 110 Cytoplasmic (Potential).  
 FT DOMAIN 1 113 Anchor for type IV membrane protein  
 FT TRANSMEM 92 110 (Potential).  
 FT DOMAIN 1 113 Vesicular (Potential).  
 FT MOD RES 1 88 N-acetylserine (By similarity).  
 FT DOMAIN 1 88 V-SNARE coiled-coil homology.  
 FT SEQUENCE 113 AA; 12341 MW; 6EC6C937B29BC6AB CRC64;



Search completed: November 1, 2004, 17:59:09  
Job time : 97.1875 secs

Query Match 97.1%; Score 168; DB 1; Length 113;  
Best Local Similarity 91.4%; Pred. No. 1.7e-16;  
Matches 32; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXPEXSAKLRKRYWKNLK 35  
DB 57 LSELDDRADALQAGASQFETSAAKLRKRYWKNMK 91

## RESULT 15

AAH60344 PRELIMINARY; PRT; 114 AA.  
AAH60344:  
02-MAR-2004 (T-EMBLrel. 27, Created)  
02-MAR-2004 (T-EMBLrel. 27, Last sequence update)  
02-MAR-2004 (T-EMBLrel. 27, Last annotation update)  
Vamp2-B-prov protein.  
VAMP2-B-PROV.  
OS Xenopus laevis (African clawed frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
OC Xenopodinae; Xenopus; Xenopus.  
NCBI\_TaxID=8355;  
[1]  
PP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX MEDLINE=22341132; PubMed=12454917;  
RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
RA Richardson P.,  
RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
RT Initiative";  
RL Dev. Dyn. 225:384-391(2002).  
[2]  
PP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RX MEDLINE=22388257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.J., Ucedin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Huiyik S.W.,  
RA Vallatou D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Keltman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smalls D.E., Schermer A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[3]  
PP SEQUENCE FROM N.A.  
RC TISSUE=Embryo;  
RA Klein S., Strausberg R.,  
RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC060344; AAH60344.1; -  
SQ SEQUENCE 114 AA; 12472 MW; AEF2EDDCDF2D1DBF CRC64;

Query Match 97.1%; Score 168; DB 2; Length 114;  
Best Local Similarity 91.4%; Pred. No. 1.7e-16;  
Matches 32; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSELDDRADALQAGASXPEXSAKLRKRYWKNLK 35  
DB 58 LSELDDRADALQAGASQFETSAAKLRKRYWKNMK 92



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 1, 2004, 17:52:26 ; Search time 108 Seconds  
(without alignments)  
139.506 Million cell updates/sec

Title: US-10-802-574-9  
Perfect score: 221  
Sequence: 1 XGJSELDPRADALQAGASQ.....TSAAKLRKRYWKNLKGSGC 42

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_23Sep04:\*  
1: geneseqp1980s:\*  
2: geneseqp1990s:\*  
3: geneseqp2000s:\*  
4: geneseqp2001s:\*  
5: geneseqp2002s:\*  
6: geneseqp2003as:\*  
7: geneseqp2003bs:\*  
8: geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	220	99.5	42	5	AA015163
2	181	81.9	40	4	AA050301
3	181	81.9	40	4	AA048582
4	181	81.9	54	3	AA039482
5	181	81.9	115	7	AA057598
6	181	81.9	115	7	AA057612
7	181	81.9	115	7	AA050831
8	181	81.9	115	7	AA057606
9	181	81.9	115	7	AA050829
10	181	81.9	115	7	AA057600
11	181	81.9	115	7	AA057604
12	181	81.9	115	7	AA057596
13	181	81.9	115	7	AA057602
14	181	81.9	115	7	AA057610
15	181	81.9	115	7	AA057592
16	181	81.9	115	7	AA057594
17	181	81.9	115	7	AA057614
18	181	81.9	115	7	AA057608
19	181	81.9	116	2	AA030104
20	181	81.9	116	2	AA043425
21	181	81.9	116	3	AA088243
22	181	81.9	116	5	AA043681
23	181	81.9	116	6	AA076220
24	181	81.9	116	6	AA036664
25	181	81.9	116	7	AA001719

26	181	81.9	116	7	AA001718	Abw01718	Mouse VAM
27	181	81.9	116	7	AA001705	Abw01705	Human VAM
28	181	81.9	116	7	AA089011	Adg89011	Bovine sy
29	181	81.9	116	8	AA097006	Adm97006	Mouse VAM
30	181	81.9	116	8	AA097007	Adm97007	Bovine VA
31	181	81.9	116	8	AA097005	Adm97005	Human VAM
32	181	81.9	368	3	AA043843	AA043843	Amino aci
33	181	81.9	368	3	AA090403	Adf90403	Rat VAMP-
34	181	81.9	608	3	AA043845	AA043845	Amino aci
35	181	81.9	609	7	AA090406	Adf90406	Rat VAMP-
36	179	81.0	82	3	AA088244	AA088244	Xenopus s
37	179	81.0	82	7	AA089012	Adg89012	Xenopus s
38	179	81.0	114	7	AA001720	Abw01720	Frog VAMP
39	179	81.0	114	8	AA097008	Adm97008	Frog VAMP
40	177	80.1	37	2	AA086822	AA086822	VAMP iso1
41	177	80.1	62	2	AA086821	AA086821	VAMP iso1
42	176	79.6	35	2	AA086824	AA086824	VAMP iso1
43	176	79.6	100	2	AA004182	AA004182	Cellubrev
44	176	79.6	100	3	AA088240	AA088240	Human cel
45	176	79.6	100	4	AA000250	AA000250	SNARE hom

## ALIGNMENTS

RESULT 1	AA015163	standard; peptide; 42 AA.
ID	AA015163	
XX	AA015163	
AC	02-SEP-2002	(first entry)
DT		
XX		
DE	Clostridial neurotoxin protease substrate peptide 2.	
XX		
KM	Clostridial neurotoxin substrate; botulinum neurotoxin substrate; FBET;	
KM	fluorescence resonant energy transfer assay; quenched-signal;	
KM	clostridial neurotoxin detection; food.	
XX		
OS	Unidentified.	
XX		
FH	Key	Location/Qualifiers
FT	Modified-site	1
FT	Cleavage-site	/note="N-fluoresceinyl-glycine"
FT		20..21
FT		/note="The peptide is cleaved between these two residues by the clostridial neurotoxin"
XX		
PN	W0200225284-A2.	
XX		
PD	28-MAR-2002.	
XX		
PF	25-SEP-2001; 2001WO-US030188.	
XX		
PR	25-SEP-2000; 2000US-0235050P.	
XX		
PA	(USME-) US MEDICAL RES INST INFECTIOUS DISEASES.	
XX		
PI	Schmidt JT, Stafford RG;	
XX		
DR	WPI; 2002-499829/53.	
XX		
PT	Substrate useful in e.g. an assay for the protease activity of	
PT	clostridial neurotoxin, comprises modified peptide or protein.	
XX		
PS	Claim 24; Page 15; 48pp; English.	
XX		
CC	The invention comprises clostridial neurotoxin substrate peptides which	
CC	can serve as fluorescence resonant energy transfer assay (FBET) or	
CC	quenched-signal substrates in assays for the proteolytic activities of	
CC	clostridial neurotoxins. The invention further comprises Clostridium	
CC	botulinum neurotoxin substrate peptides that can serve as immobilised	
CC	substrates (i.e. bound to a solid phase) in assays for the proteolytic	

activities of clostridial neurotoxins. The clostridial (including the Clostridium botulinum) neurotoxin substrate peptides are useful for detecting the presence of clostridial neurotoxins in a sample (e.g. food or an environmental sample). The present amino acid sequence represents a clostridial neurotoxin substrate peptide of the invention

Sequence 42 AA:  
Query Match 99.5%; Score 220; DB 5; Length 42;  
Best Local Similarity 100.0%; Pred. No. 8.5e-23;  
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGLSELDPRADALQAGASQFETSAKLKRYWKNLKGSGC 42  
DB 2 GGLSELDPRADALQAGASQFETSAKLKRYWKNLKGSGC 42

RESULT 2  
ID AAB50301 standard; peptide; 40 AA.

XX AAB50301;

DT 08-MAR-2001 (first entry)

XX VAMP2 peptide.

XX VAMP2; antibacterial; Botulinum toxin inhibitor; BttxB; previn;  
XX tetanus neurotoxin; buforinin.

XX Unidentified.

XX WO200069891-A2.

XX 23-NOV-2000.

XX 15-MAY-2000; 2000WO-US013215.

XX 17-MAY-1999; 99US-0134446P.

XX (USSA ) US DEPT OF THE ARMY.

XX Gordon RK, Moorad DR, Doctor BP, Garcia GE;

XX WPI; 2001-025001/03.

XX Novel Previn compounds useful for inhibiting the protease activity of  
XX Botulinum B and tetanus toxins.

XX Disclosure; Page 5; 47pp; English.

XX The present sequence was investigated in the search for Botulinum toxin  
XX inhibitors (BttxB). Previn compounds which inhibit the enzymatic activity  
XX of BttxB and tetanus neurotoxins were isolated. Previns may be used to  
XX construct compounds such as buforinins

XX Sequence 40 AA;

Query Match 81.9%; Score 181; DB 4; Length 40;  
Best Local Similarity 100.0%; Pred. No. 2e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDDRADALQAGASQFETSAKLKRYWKNLKG 38  
DB 6 LSELDDRADALQAGASQFETSAKLKRYWKNLKG 40

RESULT 3  
ID AAB48582 standard; peptide; 40 AA.

XX AAB48582;

DT 08-MAR-2001 (first entry)

XX VAMP2 peptide.

XX Buforin; Botulinum toxin B; BttxB; Tetanus neurotoxin; endoprotease;  
XX antibacterial; VAMP2; synaptobrevin.

XX Unidentified.

XX WO200069895-A2.

XX 23-NOV-2000.

XX 11-MAY-2000; 2000WO-US012909.

XX 14-MAY-1999; 99US-0134216P.

XX (USSA ) US DEPT OF THE ARMY.

XX Garcia GE, Gordon RK, Moorad DR, Doctor BP;

XX WPI; 2001-102250/11.

XX Novel peptides capable of inhibiting the enzymatic activity of Botulinum  
XX toxin B, and Tetanus neurotoxins useful for preventing or treating toxic  
XX poisoning such as Botulinum toxin and tetanus poisoning.

XX Disclosure; Page 5; 47pp; English.

XX The present sequence is one of a number of peptide or peptide-like  
XX compounds, designated buforin, which inhibit the enzymatic activity of  
XX Botulinum toxin B (BttxB) and Tetanus neurotoxins. The buforins are  
XX useful for treating Botulinum or tetanus intoxication by administering a  
XX composition comprising a buforin to the subject prior to the contact with  
XX BttxB or tetanus intoxication. Antibodies specific for buforins are  
XX useful for detecting buforins by forming immunocomplexes. The buforins  
XX have improved circulatory half-life, solubility, resistance to  
XX degradation and interaction with the active site of the toxin

XX Sequence 40 AA;

Query Match 81.9%; Score 181; DB 4; Length 40;  
Best Local Similarity 100.0%; Pred. No. 2e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDDRADALQAGASQFETSAKLKRYWKNLKG 38  
DB 6 LSELDDRADALQAGASQFETSAKLKRYWKNLKG 40

RESULT 4  
ID AAB39482 standard; protein; 54 AA.

XX AAB39482;

XX 02-FEB-2001 (first entry)

XX Gene 49 human secreted protein homologous amino acid sequence #141.

XX Human; secreted protein; diagnosis; cyrostatic; immunosuppressive;  
XX nocitropic; neuroprotective; antiviral; antiallergic; hepatotropic;  
XX antidiabetic; antiinflammatory; antiviral; vulerary; anticonvulsant;  
XX antibacterial; antifungal; antiparasitic; cardiant; gene therapy;  
XX food additive; preservative; chromosome identification; cancer;  
XX female reproductive system disorder; immune disorder; wound healing;  
XX cardiovascular disorder; neurological disease; infectious disease;  
XX infection.

XX Bos taurus.  
XX WO200058340-A2.

PD 05-OCT-2000.  
XX  
XX 23-MAR-2000; 2000WO-US007724.  
XX  
XX 26-MAR-1999; 99US-0126510P.  
PR 07-JAN-2000; 2000US-0174850P.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA  
PI Rosen CA, Ruben SM, Komatsoulis G;  
DR WPI; 2000-594638/56.  
XX  
XX Fifty nucleic acid molecules encoding human secreted proteins, useful in  
PT the prevention, treatment and diagnosis of cancer, immune disorders,  
PT cardiovascular disorders and neurological diseases.  
XX  
XX Disclosure; Page 390, 391pp; English.  
XX  
XX The polynucleotide sequences given in AAC74337 to AAC74386 encode the  
CC human secreted proteins given in AAB39402 to AAB39451. AAB39452 to  
CC AAB39484 represent human secreted polypeptide sequences and proteins  
CC homologous to them, which are given in the exemplification of the present  
CC invention. Human secreted proteins have activities based on the tissues  
CC and cells the genes are expressed in. Example of activities include:  
CC cytostatic; immunosuppressive; nootropic; neuroprotective; antiviral;  
CC antiallergic; hepatotropic; antidiabetic; antiinflammatory; antitumor;  
CC vulnary; anticonvulsant; antibacterial; antifungal; antiparasitic; and  
CC caritant. The polynucleotides and polypeptides are useful for preventing,  
CC treating or ameliorating a medical condition in e.g. humans, mice,  
CC rabbits, goats, horses, cats, dogs, chickens or sheep. The polypeptides  
CC can also be used as a food additive or preservative to increase or  
CC decrease storage capabilities. The polynucleotide are useful for  
CC chromosome identification. They are also useful as probes for diagnosing  
CC a disorder related to the female reproductive system, particularly breast  
CC and/or ovary cancer. They are also useful in the gene therapy of breast  
CC and ovarian cancer. Secreted protein nucleic acids, proteins, antibodies,  
CC agonists and antagonists are useful in the diagnosis, treatment and  
CC prevention of: (a) cancer; (b) immune disorders; (c) cardiovascular  
CC disorders; (d) wound healing; (e) neurological diseases; and (f)  
CC infectious diseases such as viral, bacterial, fungal and parasitic  
CC infections. AAC74328 to AAC74336 and AAB39401 represent sequences used in  
CC the exemplification of the present invention  
XX  
XX Sequence 54 AA;  
SQ

Query Match 81.9%; Score 181; DB 3; Length 54;  
Best Local Similarity 100.0%; Pred. No. 2.8e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 LSELDPRADALQAGASQFETSAKLRKRYKWK 38  
DB 20 LSELDPRADALQAGASQFETSAKLRKRYKWK 54

RESULT 5  
ADES7598  
ID ADES7598 standard; protein; 115 AA.  
XX  
XX ADES7598;  
AC  
XX  
XX 29-JAN-2004 (first entry)  
DT  
XX  
XX Human Protein P19065, SEQ ID NO 3460.  
DE  
XX  
XX Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.  
XX  
XX Homo sapiens.  
OS  
XX  
XX  
XX WO2003016475-A2.  
XX

PD 27-FEB-2003.  
XX  
XX 14-AUG-2002; 2002WO-US025765.  
PF  
XX  
XX 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX  
XX (GENO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
XX  
PI Woolf C, D'urso D, Befort K, Costigan M;  
DR WPI; 2003-268312/26.  
DR GENBANK; P19065.  
XX  
XX New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
PT  
XX  
XX Claim 1, Page; 1017pp; English.  
XX  
XX The invention discloses a composition comprising two or more isolated rat  
CC or human polynucleotides or a polynucleotide which represents a fragment,  
CC derivative or allelic variation of the nucleic acid sequence. Also  
CC claimed are a vector comprising the novel polynucleotide, a host cell  
CC comprising the vector, a method for identifying a nucleotide sequence  
CC which is differentially regulated in an animal subjected to pain and a  
CC kit to perform the method, an array, a method for identifying an agent  
CC that increases or decreases the expression of the polynucleotide sequence  
CC that is differentially expressed in neuronal tissue of a first animal  
CC subjected to pain, a method for identifying a compound which regulates  
CC the expression of a polynucleotide sequence which is differentially  
CC expressed in an animal subjected to pain, a method for identifying a  
CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antibodies. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pat\_sequences.  
XX  
XX Sequence 115 AA;  
SQ

Query Match 81.9%; Score 181; DB 7; Length 115;  
Best Local Similarity 100.0%; Pred. No. 6.6e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 LSELDPRADALQAGASQFETSAKLRKRYKWK 38  
DB 59 LSELDPRADALQAGASQFETSAKLRKRYKWK 93

RESULT 6  
ADES7612  
ID ADES7612 standard; protein; 115 AA.  
XX  
XX ADES7612;  
AC  
XX  
XX 29-JAN-2004 (first entry)  
DT  
XX  
XX Rat Protein Q64357, SEQ ID NO 3474.  
DE  
XX  
XX Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
KW  
XX

OS Rattus norvegicus.  
PN WO2003016475-A2.  
XX  
XX 27-FEB-2003.  
PD  
PF 14-AUG-2002; 2002WO-US025765.  
XX  
XX 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX  
PA (GEHO ) GEN HOSPITAL CORP.  
PA (FARB ) BAYER AG.  
XX  
XX Woolf C, D'urso D, Befort K, Costigan M;  
XX WPI; 2003-268312/26.  
DR GENBANK; Q64357.  
XX  
XX  
PT New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
XX  
XX  
PS Claim 1; Page: 1017pp; English.  
XX  
XX The invention discloses a composition comprising two or more isolated rat  
XX or human polynucleotides or a polynucleotide which represents a fragment,  
XX derivative or allelic variation of the nucleic acid sequence. Also  
XX claimed are a vector comprising the novel polynucleotide, a host cell  
XX comprising the vector, a method for identifying a nucleotide sequence  
XX which is differentially regulated in an animal subjected to pain and a  
XX kit to perform the method, an array, a method for identifying an agent  
XX that increases or decreases the expression of the polynucleotide sequence  
XX that is differentially expressed in neuronal tissue of a first animal  
XX subjected to pain, a method for identifying a compound which regulates  
XX the expression of a polynucleotide sequence which is differentially  
XX expressed in an animal subjected to pain, a method for identifying a  
XX compound that regulates the activity of one or more of the  
XX polynucleotides, a method for producing a pharmaceutical composition, a  
XX method for identifying a compound or small molecule that regulates the  
XX activity in an animal of one or more of the polypeptides given in the  
XX specification, a method for identifying a compound useful in treating  
XX pain and a pharmaceutical composition comprising the one or more  
XX polypeptides or their antibodies. The polynucleotide or the compound that  
XX modulates its activity is useful for preparing a medicament for treating  
XX pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
XX therapy). The sequence presented is a rat protein (shown in Table 2 of  
XX the specification) which is differentially expressed during pain. Note:  
XX The sequence data for this patent did not form part of the printed  
XX specification, but was obtained in electronic form directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 115 AA;  
XX  
XX Query Match 81.9%; Score 181; DB 7; Length 115;  
XX Best Local Similarity 100.0%; Pred. No. 6.6e-17;  
XX Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 LSELDPRADALQAGASQFETSAKTKRKYWKXK 38  
DB 59 LSELDPRADALQAGASQFETSAKTKRKYWKXK 93  
ID ADE60831 standard; protein; 115 AA.  
XX  
XX ADE60831;  
AC  
XX  
XX 29-JAN-2004 (first entry)  
DT Human Protein P19065, SEQ ID NO 6743.  
XX  
XX

XX Human; pain; neuronal tissue; gene therapy;  
XX spinal segmental nerve injury; chronic constriction injury; CCI;  
XX spared nerve injury; SNI; Chung.  
XX  
XX Homo sapiens.  
XX WO2003016475-A2.  
XX  
XX 27-FEB-2003.  
XX  
XX 14-AUG-2002; 2002WO-US025765.  
XX  
XX 14-AUG-2001; 2001US-0312147P.  
XX 01-NOV-2001; 2001US-0346382P.  
XX 26-NOV-2001; 2001US-0333347P.  
XX  
XX (GEHO ) GEN HOSPITAL CORP.  
XX (FARB ) BAYER AG.  
XX  
XX Woolf C, D'urso D, Befort K, Costigan M;  
XX WPI; 2003-268312/26.  
XX GENBANK; P19065.  
XX  
XX  
PT New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
XX  
XX  
PS Claim 1; Page: 1017pp; English.

XX The invention discloses a composition comprising two or more isolated rat  
XX or human polynucleotides or a polynucleotide which represents a fragment,  
XX derivative or allelic variation of the nucleic acid sequence. Also  
XX claimed are a vector comprising the novel polynucleotide, a host cell  
XX comprising the vector, a method for identifying a nucleotide sequence  
XX which is differentially regulated in an animal subjected to pain and a  
XX kit to perform the method, an array, a method for identifying an agent  
XX that increases or decreases the expression of the polynucleotide sequence  
XX that is differentially expressed in neuronal tissue of a first animal  
XX subjected to pain, a method for identifying a compound which regulates  
XX the expression of a polynucleotide sequence which is differentially  
XX expressed in an animal subjected to pain, a method for identifying a  
XX compound that regulates the activity of one or more of the  
XX polynucleotides, a method for producing a pharmaceutical composition, a  
XX method for identifying a compound or small molecule that regulates the  
XX activity in an animal of one or more of the polypeptides given in the  
XX specification, a method for identifying a compound useful in treating  
XX pain and a pharmaceutical composition comprising the one or more  
XX polypeptides or their antibodies. The polynucleotide or the compound that  
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XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
XX therapy). The sequence presented is a human protein (shown in Table 2 of  
XX the specification) which is differentially expressed during pain. Note:  
XX The sequence data for this patent did not form part of the printed  
XX specification, but was obtained in electronic form directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 115 AA;  
XX

OY 4 LSELDPRADALQAGASQFETSAKTKRKYWKXK 38  
DB 59 LSELDPRADALQAGASQFETSAKTKRKYWKXK 93  
ID ADE57606 standard; protein; 115 AA.  
XX  
XX ADE57606;  
AC  
XX  
XX 29-JAN-2004 (first entry)  
DT Human Protein P19065, SEQ ID NO 6743.  
XX  
XX

AC ADE57606;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Human Protein P19065, SEQ ID NO 3468.  
XX  
KW Human; pain; neuronal tissue; gene therapy;  
KW spinal segmental nerve injury; chronic constriction injury; CCI;  
KW spared nerve injury; SNI; Chung.  
XX  
OS Homo sapiens.  
XX  
FN WO2003016475-A2.  
XX  
PD 27-FEB-2003.  
XX  
PF 14-AUG-2002; 2002MO-US025765.  
XX  
PR 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX  
PA (GENO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
PI Woolf C, D'urso D, Befort K, Costigan M;  
XX  
XX WPI; 2003-268312/26.  
DR GENBANK; P19065.  
DR  
PT New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
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XX The invention discloses a composition comprising two or more isolated rat  
XX or human polynucleotides or a polynucleotide which represents a fragment,  
XX derivative or allelic variation of the nucleic acid sequence. Also  
XX claimed are a vector comprising the novel polynucleotide, a host cell  
XX comprising the vector, a method for identifying a nucleotide sequence  
XX which is differentially regulated in an animal subjected to pain and a  
XX kit to perform the method, an array, a method for identifying an agent  
XX that increases or decreases the expression of the polynucleotide sequence  
XX that is differentially expressed in neuronal tissue of a first animal  
XX subjected to pain, a method for identifying a compound which regulates  
XX the expression of a polynucleotide sequence which is differentially  
XX expressed in an animal subjected to pain, a method for identifying a  
XX compound that regulates the activity of one or more of the  
XX polynucleotides, a method for producing a pharmaceutical composition, a  
XX method for identifying a compound or small molecule that regulates the  
XX activity in an animal of one or more of the polypeptides given in the  
XX specification, a method for identifying a compound useful in treating  
XX pain and a pharmaceutical composition comprising the one or more  
XX polypeptides or their antibodies. The polynucleotide or the compound that  
XX modulates its activity is useful for preparing a medicament for treating  
XX pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
XX therapy). The sequence presented is a human protein (shown in Table 2 of  
XX the specification) which is differentially expressed during pain. Note:  
XX The sequence data for this patent did not form part of the printed  
XX specification, but was obtained in electronic form directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 115 AA;  
XX  
Query Match 81.9%; Score 181; DB 7; Length 115;  
Best Local Similarity 100.0%; Pred. No. 6.6e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 9  
ADE60829  
ID ADE60829 standard; protein; 115 AA.  
XX  
AC ADE60829;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Rat Protein Q64357, SEQ ID NO 6741.  
XX  
KW Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
KW chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
XX  
OS Rattus norvegicus.  
XX  
FN WO2003016475-A2.  
XX  
PD 27-FEB-2003.  
XX  
PF 14-AUG-2002; 2002MO-US025765.  
XX  
PR 14-AUG-2001; 2001US-0312147P.  
PR 01-NOV-2001; 2001US-0346382P.  
PR 26-NOV-2001; 2001US-0333347P.  
XX  
PA (GENO) GEN HOSPITAL CORP.  
PA (FARB) BAYER AG.  
PI Woolf C, D'urso D, Befort K, Costigan M;  
XX  
XX WPI; 2003-268312/26.  
DR GENBANK; Q64357.  
DR  
PT New composition comprising two or more isolated polypeptides, useful for  
PT preparing a medicament for treating pain in an animal.  
XX  
PS Claim 1, Page; 1017pp; English.  
XX  
XX The invention discloses a composition comprising two or more isolated rat  
XX or human polynucleotides or a polynucleotide which represents a fragment,  
XX derivative or allelic variation of the nucleic acid sequence. Also  
XX claimed are a vector comprising the novel polynucleotide, a host cell  
XX comprising the vector, a method for identifying a nucleotide sequence  
XX which is differentially regulated in an animal subjected to pain and a  
XX kit to perform the method, an array, a method for identifying an agent  
XX that increases or decreases the expression of the polynucleotide sequence  
XX that is differentially expressed in neuronal tissue of a first animal  
XX subjected to pain, a method for identifying a compound which regulates  
XX the expression of a polynucleotide sequence which is differentially  
XX expressed in an animal subjected to pain, a method for identifying a  
XX compound that regulates the activity of one or more of the  
XX polynucleotides, a method for producing a pharmaceutical composition, a  
XX method for identifying a compound or small molecule that regulates the  
XX activity in an animal of one or more of the polypeptides given in the  
XX specification, a method for identifying a compound useful in treating  
XX pain and a pharmaceutical composition comprising the one or more  
XX polypeptides or their antibodies. The polynucleotide or the compound that  
XX modulates its activity is useful for preparing a medicament for treating  
XX pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
XX injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
XX therapy). The sequence presented is a rat protein (shown in Table 2 of  
XX the specification) which is differentially expressed during pain. Note:  
XX The sequence data for this patent did not form part of the printed  
XX specification, but was obtained in electronic form directly from WIPO at  
XX ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 115 AA;  
XX  
Query Match 81.9%; Score 181; DB 7; Length 115;  
Best Local Similarity 100.0%; Pred. No. 6.6e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDDRADALQAGASQFETSAKLKRYKWMXNLK 38  
 DB 59 LSELDDRADALQAGASQFETSAKLKRYKWMXNLK 93

## RESULT 10

AD557600  
 ADE57600 standard; protein; 115 AA.

AD557600;  
 29-JAN-2004 (first entry)

Rat Protein Q64357, SEQ ID NO 3462.

Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
 chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

Rattus norvegicus.

WO2003016475-A2.

27-FEB-2003.

14-AUG-2002; 2002WO-US025765.

14-AUG-2001; 2001US-0312147P.

01-NOV-2001; 2001US-0346382P.

26-NOV-2001; 2001US-0333347P.

(GENO) GEN HOSPITAL CORP.

(FARB) BAYER AG.

Wolff C, D'urso D, Befort K, Costigan M;  
 WPI: 2003-268312/26.

GENBANK; Q64357.

New composition comprising two or more isolated polypeptides, useful for  
 preparing a medicament for treating pain in an animal.

Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat  
 or human polynucleotides or a polynucleotide which represents a fragment,  
 derivative or allelic variation of the nucleic acid sequence. Also  
 claimed are a vector comprising the novel polynucleotide, a host cell  
 comprising the vector, a method for identifying a nucleotide sequence  
 which is differentially regulated in an animal subjected to pain and a  
 kit to perform the method, an array, a method for identifying an agent  
 that increases or decreases the expression of the polynucleotide sequence  
 that is differentially expressed in neuronal tissue of a first animal  
 subjected to pain, a method for identifying a compound which regulates  
 the expression of a polynucleotide sequence which is differentially  
 expressed in an animal subjected to pain, a method for identifying a  
 compound that regulates the activity of one or more of the  
 polynucleotides, a method for producing a pharmaceutical composition, a  
 method for identifying a compound or small molecule that regulates the  
 activity in an animal of one or more of the polypeptides given in the  
 specification, a method for identifying a compound useful in treating  
 pain and a pharmaceutical composition comprising the one or more  
 polypeptides or their antibodies. The polynucleotide or the compound that  
 modulates its activity is useful for preparing a medicament for treating  
 pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
 injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 therapy). The sequence presented is a rat protein (shown in Table 2 of  
 the specification) which is differentially expressed during pain. Note:  
 The sequence data for this patent did not form part of the printed  
 specification, but was obtained in electronic form directly from WIPO at  
 ftp.wipo.int/pub/published\_pct\_sequences.

Query Match 81.9%; Score 181; DB 7; Length 115;  
 Best Local Similarity 100.0%; Pred. No. 6,6e-17;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDDRADALQAGASQFETSAKLKRYKWMXNLK 38  
 DB 59 LSELDDRADALQAGASQFETSAKLKRYKWMXNLK 93

## RESULT 11

AD557604  
 ADE57604 standard; protein; 115 AA.

AD557604;  
 29-JAN-2004 (first entry)

Rat Protein Q64357, SEQ ID NO 3466.

Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
 chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

Rattus norvegicus.

WO2003016475-A2.

27-FEB-2003.

14-AUG-2002; 2002WO-US025765.

14-AUG-2001; 2001US-0312147P.

01-NOV-2001; 2001US-0346382P.

26-NOV-2001; 2001US-0333347P.

(GENO) GEN HOSPITAL CORP.

(FARB) BAYER AG.

Wolff C, D'urso D, Befort K, Costigan M;  
 WPI: 2003-268312/26.

GENBANK; Q64357.

New composition comprising two or more isolated polypeptides, useful for  
 preparing a medicament for treating pain in an animal.

Claim 1; Page; 1017pp; English.

The invention discloses a composition comprising two or more isolated rat  
 or human polynucleotides or a polynucleotide which represents a fragment,  
 derivative or allelic variation of the nucleic acid sequence. Also  
 claimed are a vector comprising the novel polynucleotide, a host cell  
 comprising the vector, a method for identifying a nucleotide sequence  
 which is differentially regulated in an animal subjected to pain and a  
 kit to perform the method, an array, a method for identifying an agent  
 that increases or decreases the expression of the polynucleotide sequence  
 that is differentially expressed in neuronal tissue of a first animal  
 subjected to pain, a method for identifying a compound which regulates  
 the expression of a polynucleotide sequence which is differentially  
 expressed in an animal subjected to pain, a method for identifying a  
 compound that regulates the activity of one or more of the  
 polynucleotides, a method for producing a pharmaceutical composition, a  
 method for identifying a compound or small molecule that regulates the  
 activity in an animal of one or more of the polypeptides given in the  
 specification, a method for identifying a compound useful in treating  
 pain and a pharmaceutical composition comprising the one or more  
 polypeptides or their antibodies. The polynucleotide or the compound that  
 modulates its activity is useful for preparing a medicament for treating  
 pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
 injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
 therapy). The sequence presented is a rat protein (shown in Table 2 of  
 the specification) which is differentially expressed during pain. Note:  
 The sequence data for this patent did not form part of the printed  
 specification, but was obtained in electronic form directly from WIPO at

CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 115 AA;  
 Query Match 81.9%; Score 181; DB 7; Length 115;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-17;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LSEDDRADALQAGASQFETSAKLRKRYWKNLK 38  
 |||||  
 Db 59 LSEDDRADALQAGASQFETSAKLRKRYWKNLK 93

RESULT 12  
 ADE57596  
 ID ADE57596 standard; protein; 115 AA.  
 XX ADE57596;  
 AC  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Rat Protein Q64357, SEQ ID NO 3458.  
 XX  
 KM Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;  
 KM chronic constriction injury; CCI; spared nerve injury; SNI; Chung.  
 XX  
 OS Rattus norvegicus.  
 XX  
 PN WO2003016475-A2.  
 XX  
 PD 27-FEB-2003.  
 XX  
 PF 14-AUG-2002; 2002WO-US025765.  
 XX  
 PR 14-AUG-2001; 2001US-0312147P.  
 PR 01-NOV-2001; 2001US-0346382P.  
 PR 26-NOV-2001; 2001US-0333347P.  
 XX  
 PA (GEHO ) GEN HOSPITAL CORP.  
 PA (FARB ) BAYER AG.  
 XX  
 PI Woolf C, D'urso D, Befort K, Costigan M;  
 XX  
 DR WPI; 2003-268312/26.  
 DR GENBANK; Q64357.  
 XX  
 PT New composition comprising two or more isolated polypeptides, useful for  
 PT preparing a medicament for treating pain in an animal.  
 XX  
 PS Claim 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat  
 CC or human polynucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC claimed are a vector comprising the novel polynucleotide, a host cell  
 CC comprising the vector, a method for identifying a nucleotide sequence  
 CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying an agent  
 CC that increases or decreases the expression of the polynucleotide sequence  
 CC that is differentially expressed in neuronal tissue of a first animal  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating  
 CC pain and a pharmaceutical composition comprising the one or more  
 CC polypeptides or their antibodies. The polynucleotide or the compound that  
 CC modulates its activity is useful for preparing a medicament for treating  
 CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
 CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene

CC therapy). The sequence presented is a rat protein (shown in Table 2 of  
 CC the specification) which is differentially expressed during pain. Note:  
 CC The sequence data for this patent did not form part of the printed  
 CC specification, but was obtained in electronic form directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 115 AA;  
 Query Match 81.9%; Score 181; DB 7; Length 115;  
 Best Local Similarity 100.0%; Pred. No. 6.6e-17;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LSEDDRADALQAGASQFETSAKLRKRYWKNLK 38  
 |||||  
 Db 59 LSEDDRADALQAGASQFETSAKLRKRYWKNLK 93

RESULT 13  
 ADE57602  
 ID ADE57602 standard; protein; 115 AA.  
 XX ADE57602;  
 AC  
 XX  
 DT 29-JAN-2004 (first entry)  
 XX  
 DE Human Protein P19065, SEQ ID NO 3464.  
 XX  
 KM Human; pain; neuronal tissue; gene therapy;  
 KM spinal segmental nerve injury; chronic constriction injury; CCI;  
 KM spared nerve injury; SNI; Chung.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003016475-A2.  
 XX  
 PD 27-FEB-2003.  
 XX  
 PF 14-AUG-2002; 2002WO-US025765.  
 XX  
 PR 14-AUG-2001; 2001US-0312147P.  
 PR 01-NOV-2001; 2001US-0346382P.  
 PR 26-NOV-2001; 2001US-0333347P.  
 XX  
 PA (GEHO ) GEN HOSPITAL CORP.  
 PA (FARB ) BAYER AG.  
 XX  
 PI Woolf C, D'urso D, Befort K, Costigan M;  
 XX  
 DR WPI; 2003-268312/26.  
 DR GENBANK; P19065.  
 XX  
 PT New composition comprising two or more isolated polypeptides, useful for  
 PT preparing a medicament for treating pain in an animal.  
 XX  
 PS Claim 1; Page; 1017pp; English.

CC The invention discloses a composition comprising two or more isolated rat  
 CC or human polynucleotides or a polynucleotide which represents a fragment,  
 CC derivative or allelic variation of the nucleic acid sequence. Also  
 CC claimed are a vector comprising the novel polynucleotide, a host cell  
 CC comprising the vector, a method for identifying a nucleotide sequence  
 CC which is differentially regulated in an animal subjected to pain and a  
 CC kit to perform the method, an array, a method for identifying an agent  
 CC that increases or decreases the expression of the polynucleotide sequence  
 CC that is differentially expressed in neuronal tissue of a first animal  
 CC subjected to pain, a method for identifying a compound which regulates  
 CC the expression of a polynucleotide sequence which is differentially  
 CC expressed in an animal subjected to pain, a method for identifying a  
 CC compound that regulates the activity of one or more of the  
 CC polynucleotides, a method for producing a pharmaceutical composition, a  
 CC method for identifying a compound or small molecule that regulates the  
 CC activity in an animal of one or more of the polypeptides given in the  
 CC specification, a method for identifying a compound useful in treating



CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antipeptides. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 115 AA;

XX Query Match 81.9%; Score 181; DB 7; Length 115;

XX Best Local Similarity 100.0%; Pred. No. 6,6e-17;

XX Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 4 LSELDPRADALQAGASQFETSAKTKRKYWKXK 38  
XX 59 LSELDPRADALQAGASQFETSAKTKRKYWKXK 93

XX RESULT 14

XX ID: ADE57610 standard; protein; 115 AA.

XX AC: ADE57610;

XX DT: 29-JAN-2004 (first entry)

XX DE: Human Protein P19065, SEQ ID NO 3472.

XX KW: Human; pain; neuronal tissue; gene therapy;

XX KW: spinal segmental nerve injury; chronic constriction injury; CCI;

XX KW: spared nerve injury; SNI; Chung.

XX OS: Homo sapiens.

XX PN: WO2003016475-A2.

XX PD: 27-FEB-2003.

XX PF: 14-AUG-2002; 2002MO-US025765.

XX PR: 14-AUG-2001; 2001US-0312147P.

XX PR: 01-NOV-2001; 2001US-0346382P.

XX PR: 26-NOV-2001; 2001US-0333347P.

XX PA: (GENO ) GEN HOSPITAL CORP.

XX PA: (FARB ) BAYER AG.

XX PI: Woolf C, D'Urso D, Befort K, Costigan M;

XX WP: 2003-268312/26.

XX GENBANK; P19065.

XX Claim 1; Page: 1017p; English.

XX The invention discloses a composition comprising two or more isolated rat  
XX or human polynucleotides or a polynucleotide which represents a fragment,  
XX derivative or allelic variation of the nucleic acid sequence. Also  
XX claimed are a vector comprising the novel polynucleotide, a host cell  
XX comprising the vector, a method for identifying a nucleotide sequence  
XX which is differentially regulated in an animal subjected to pain and a  
XX kit to perform the method, an array, a method for identifying an agent  
XX that increases or decreases the expression of the polynucleotide sequence  
XX that is differentially expressed in neuronal tissue of a first animal  
XX subjected to pain, a method for identifying a compound which regulates  
XX the expression of a polynucleotide sequence which is differentially  
XX expressed in an animal subjected to pain, a method for identifying a

CC compound that regulates the activity of one or more of the  
CC polynucleotides, a method for producing a pharmaceutical composition, a  
CC method for identifying a compound or small molecule that regulates the  
CC activity in an animal of one or more of the polypeptides given in the  
CC specification, a method for identifying a compound useful in treating  
CC pain and a pharmaceutical composition comprising the one or more  
CC polypeptides or their antipeptides. The polynucleotide or the compound that  
CC modulates its activity is useful for preparing a medicament for treating  
CC pain (e.g. spinal segmental nerve injury (Chung), chronic constriction  
CC injury (CCI) and spared nerve injury (SNI)) in an animal (e.g. gene  
CC therapy). The sequence presented is a human protein (shown in Table 2 of  
CC the specification) which is differentially expressed during pain. Note:  
CC The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic form directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 115 AA;

XX Query Match 81.9%; Score 181; DB 7; Length 115;

XX Best Local Similarity 100.0%; Pred. No. 6,6e-17;

XX Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX 4 LSELDPRADALQAGASQFETSAKTKRKYWKXK 38  
XX 59 LSELDPRADALQAGASQFETSAKTKRKYWKXK 93

XX RESULT 15

XX ID: ADE57592 standard; protein; 115 AA.

XX AC: ADE57592;

XX DT: 29-JAN-2004 (first entry)

XX DE: Rat Protein Q64357, SEQ ID NO 3454.

XX KW: Rat; pain; neuronal tissue; gene therapy; spinal segmental nerve injury;

XX KW: chronic constriction injury; CCI; spared nerve injury; SNI; Chung.

XX OS: Rattus norvegicus.

XX PN: WO2003016475-A2.

XX PD: 27-FEB-2003.

XX PF: 14-AUG-2002; 2002MO-US025765.

XX PR: 14-AUG-2001; 2001US-0312147P.

XX PR: 01-NOV-2001; 2001US-0346382P.

XX PR: 26-NOV-2001; 2001US-0333347P.

XX PA: (GENO ) GEN HOSPITAL CORP.

XX PA: (FARB ) BAYER AG.

XX PI: Woolf C, D'Urso D, Befort K, Costigan M;

XX WP: 2003-268312/26.

XX GENBANK; Q64357.

XX Claim 1; Page: 1017p; English.

XX The invention discloses a composition comprising two or more isolated rat  
XX or human polynucleotides or a polynucleotide which represents a fragment,  
XX derivative or allelic variation of the nucleic acid sequence. Also  
XX claimed are a vector comprising the novel polynucleotide, a host cell  
XX comprising the vector, a method for identifying a nucleotide sequence  
XX which is differentially regulated in an animal subjected to pain and a  
XX kit to perform the method, an array, a method for identifying an agent  
XX that increases or decreases the expression of the polynucleotide sequence





2

Tue Nov 2 10:45:15 2004

us-10-802-574-9.ra1

Page 1

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OM protein - protein search, using sw model

Run on: November 1, 2004, 17:53:05 ; Search time 28.125 Seconds  
(Without alignments)  
99.035 Million cell updates/sec

Title: US-10-802-574-9  
Perfect score: 221  
Sequence: 1 XGISELDRADALQAGASQ.....TSAAKLKRYWKNLKGSGC 42

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 6631800 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/1aa/5B.COMB.rep.\*  
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6: /cgn2\_6/ptodata/1/1aa/backfile1est.rep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	181	81.9	35	2	US-08-760-001-11
3	181	81.9	35	3	US-09-015-960-11
4	181	81.9	35	3	US-09-534-572-11
5	181	81.9	40	4	US-09-570-022-16
6	181	81.9	40	4	US-09-570-023-8
7	181	81.9	116	1	US-08-409-373B-4
8	181	81.9	116	1	US-08-409-373B-4
9	181	81.9	116	1	US-08-393-985-16
10	181	81.9	116	3	US-08-621-018B-10
11	181	81.9	116	3	US-08-813-266-2
12	181	81.9	116	3	US-09-483-665-10
13	179	81.0	82	4	US-08-621-018B-11
14	179	81.0	82	4	US-09-483-665-11
15	177	80.1	35	2	US-08-760-001-9
16	177	80.1	35	3	US-09-015-960-9
17	177	80.1	35	3	US-09-534-572-9
18	177	80.1	62	2	US-08-760-001-8
19	177	80.1	62	2	US-09-015-960-8
20	177	80.1	62	3	US-09-534-572-8
21	176	79.6	100	3	US-08-621-018B-6
22	176	79.6	100	4	US-09-483-665-6
23	176	79.6	103	1	US-08-409-373B-3
24	176	79.6	103	1	US-08-409-373B-3
25	176	79.6	103	3	US-08-621-018B-9
26	176	79.6	103	4	US-09-483-665-9
27	176	79.6	347	4	US-09-513-783A-28

28	176	79.6	347	4	US-09-430-656-30	Sequence 30, Appl
29	176	79.6	350	4	US-09-513-783A-30	Sequence 30, Appl
30	176	79.6	350	4	US-09-430-656-28	Sequence 28, Appl
31	170	76.9	35	4	US-09-962-360B-4	Sequence 4, Appl
32	169	76.5	35	4	US-09-962-360B-3	Sequence 3, Appl
33	165	74.7	118	1	US-08-393-985-14	Sequence 14, Appl
34	117	52.9	56	3	US-08-813-266-5	Sequence 5, Appl
35	104	47.1	94	4	US-09-621-976-6274	Sequence 6274, Ap
36	93	42.1	20	3	US-08-813-266-13	Sequence 13, Appl
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38	88	39.8	86	4	US-09-513-999C-5451	Sequence 5451, Ap
39	88	39.8	102	1	US-08-409-373B-2	Sequence 2, Appl
40	88	39.8	102	1	US-08-409-373B-2	Sequence 2, Appl
41	88	39.8	102	3	US-08-621-018B-2	Sequence 2, Appl
42	88	39.8	102	4	US-09-483-665-2	Sequence 2, Appl
43	82.5	37.3	46	4	US-09-962-360B-10	Sequence 10, Appl
44	76	34.4	141	3	US-08-621-018B-8	Sequence 8, Appl
45	76	34.4	141	4	US-09-483-665-8	Sequence 8, Appl

## ALIGNMENTS

```
RESULT 1
US-09-962-360B-9
; Sequence 9, Application US/09962360B
; Patent No. 6762280
; GENERAL INFORMATION:
; /
; APPLICANT: Schmidt, James J.
; APPLICANT: Stafford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostridi
; TITLE OF INVENTION: Neurotoxins
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/09/962,360B
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 9
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BoNT B
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: Xaa at 1 is N-Fluoresceinyl-glycine
US-09-962-360B-9

Query Match          99.5%: Score 220; DB 4; Length 42;
Best Local Similarity 100.0%: Pred. No. 1.4e-22;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      2  GGLSELDRADALQAGASQFETSAALKRKYWKNLKGSGC 42
Db      2  GGLSELDRADALQAGASQFETSAALKRKYWKNLKGSGC 42

RESULT 2
US-08-760-001-11
; Sequence 11, Application US/08760001
; Patent No. 5962637
; GENERAL INFORMATION:
; APPLICANT: Shone, Clifford C.
; APPLICANT: Hallis, Bassam
; APPLICANT: James, Benjamin A. F.
; APPLICANT: Quinn, Conrad P.
; TITLE OF INVENTION: TOXIN ASSAY
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESSES:
```

ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/760,001  
FILING DATE: Herewith  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB95/01279  
FILING DATE: 02-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1581.0120001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2543  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-760-001-11

Query Match 81.9%; Score 181; DB 2; Length 35;  
Best Local Similarity 100.0%; Pred. No. 1.9e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDPRADALQAGASQFETSAKLRKRYWKXK 38  
DB 1 LSELDPRADALQAGASQFETSAKLRKRYWKXK 35

RESULT 3  
US-09-015-960-11  
Sequence 11, Application US/09015960  
Patent No. 6043042  
GENERAL INFORMATION:  
APPLICANT: Shone, Clifford C.  
APPLICANT: Hallis, Bassam  
APPLICANT: James, Benjamin A. F.  
APPLICANT: Quinn, Conrad P.  
TITLE OF INVENTION: TOXIN ASSAY  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/015,960  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/760,001  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1581.0120001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2543  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-015-960-11

Query Match 81.9%; Score 181; DB 3; Length 35;  
Best Local Similarity 100.0%; Pred. No. 1.9e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDPRADALQAGASQFETSAKLRKRYWKXK 38  
DB 1 LSELDPRADALQAGASQFETSAKLRKRYWKXK 35

RESULT 4  
US-09-534-572-11  
Sequence 11, Application US/09534572  
Patent No. 6337386  
GENERAL INFORMATION:  
APPLICANT: Shone, Clifford C.  
APPLICANT: Hallis, Bassam  
APPLICANT: James, Benjamin A. F.  
APPLICANT: Quinn, Conrad P.  
TITLE OF INVENTION: TOXIN ASSAY  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/534,572  
FILING DATE: Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 09/015,960  
FILING DATE: 30-JAN-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/760,001  
FILING DATE: 30-DEC-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB95/01279  
FILING DATE: 02-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1581.0120003  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2543  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 amino acids  
TYPE: amino acid  
STRANDEDNESS: single

TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-09-574-572-11

Query Match 81.9%; Score 181; DB 3; Length 35;  
Best Local Similarity 100.0%; Pred. No. 1.9e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LSELDDRADALQAGASQFETSAKLKRYWKNLK 38  
Db 1 LSELDDRADALQAGASQFETSAKLKRYWKNLK 35

RESULT 5  
US-09-570-022-16  
Sequence 16, Application US/09570022  
Patent No. 6573344  
GENERAL INFORMATION:  
APPLICANT: GORDON, RICHARD K.  
APPLICANT: MOORAD, DEBORAH R.  
APPLICANT: DOCTOR, BHUPENDRA P.  
APPLICANT: GARCIA, GREGORY E.  
TITLE OF INVENTION: PREVIOUS AS SPECIFIC INHIBITORS AND THERAPEUTIC AGENTS  
TITLE OF INVENTION: FOR BOTULINUM TOXIN B AND TETANUS NEUROTOXINS  
FILE REFERENCE: 38644-170531  
CURRENT APPLICATION NUMBER: US/09/570,022  
CURRENT FILING DATE: 2000-05-12  
PRIOR APPLICATION NUMBER: 60/134,446  
PRIOR FILING DATE: 1999-05-17  
NUMBER OF SEQ ID NOS: 26  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 16  
LENGTH: 40  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-570-022-16

Query Match 81.9%; Score 181; DB 4; Length 40;  
Best Local Similarity 100.0%; Pred. No. 2.2e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LSELDDRADALQAGASQFETSAKLKRYWKNLK 38  
Db 6 LSELDDRADALQAGASQFETSAKLKRYWKNLK 40

RESULT 6  
US-09-570-023-8  
Sequence 8, Application US/09570023  
Patent No. 6713444  
GENERAL INFORMATION:  
APPLICANT: GARCIA, GREGORY E.  
APPLICANT: GORDON, RICHARD K.  
APPLICANT: MOORAD, DEBBIE R.  
APPLICANT: DOCTOR, BHUPENDRA P.  
TITLE OF INVENTION: BUFORIN I AS A SPECIFIC INHIBITOR AND THERAPEUTIC AGENT  
TITLE OF INVENTION: FOR BOTULINUM TOXIN B AND TETANUS NEUROTOXINS  
FILE REFERENCE: 37833-20004.00  
CURRENT APPLICATION NUMBER: US/09/570,023  
CURRENT FILING DATE: 2000-05-12  
NUMBER OF SEQ ID NOS: 14  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 8  
LENGTH: 40  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-570-023-8

Query Match 81.9%; Score 181; DB 4; Length 40;  
Best Local Similarity 100.0%; Pred. No. 2.2e-17;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 4 LSELDDRADALQAGASQFETSAKLKRYWKNLK 38  
Db 6 LSELDDRADALQAGASQFETSAKLKRYWKNLK 40

RESULT 7  
US-08-409-373B-4  
Sequence 4, Application US/08409373B  
Patent No. 5585240  
GENERAL INFORMATION:  
APPLICANT: Stuart, Susan G.  
APPLICANT: Hawkins, Phillip R.  
APPLICANT: Sellhammer, Jeffrey J.  
TITLE OF INVENTION: CELLUBREVIN HOMOLOG  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/409,373B  
FILING DATE: 23-MAR-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0029 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-852-0195  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 116 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: X76199  
US-08-409-373B-4

Query Match 81.9%; Score 181; DB 1; Length 116;  
Best Local Similarity 100.0%; Pred. No. 7.2e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LSELDDRADALQAGASQFETSAKLKRYWKNLK 38  
Db 60 LSELDDRADALQAGASQFETSAKLKRYWKNLK 94

RESULT 8  
US-08-409-373B-4  
Sequence 4, Application US/08409373B  
Patent No. 5650280  
Patent No. 5650280 5585240  
GENERAL INFORMATION:  
APPLICANT: Stuart, Susan G.  
APPLICANT: Hawkins, Phillip R.  
APPLICANT: Sellhammer, Jeffrey J.  
TITLE OF INVENTION: CELLUBREVIN HOMOLOG  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/409,373B  
FILING DATE: 23-MAR-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Luther, Barbara J  
REGISTRATION NUMBER: 33,954  
REFERENCE/DOCKET NUMBER: PF-0029 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0195  
TELEFAX: 415-855-0555  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 116 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: X76199  
US-08-409-373B-4

Query Match 81.9%; Score 181; DB 1; Length 116;  
Best Local Similarity 100.0%; Pred. No. 7.2e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 38  
DB 60 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 94

RESULT 9  
US-08-393-985-16  
Sequence 16, Application US/08393985  
Patent No. 5693476  
GENERAL INFORMATION:  
APPLICANT: Scheller, Richard H.  
TITLE OF INVENTION: Methods and Compositions for Modulation  
TITLE OF INVENTION: of Vesicular Release  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Dehlinger & Associates  
STREET: 350 Cambridge Avenue, Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/393,985  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Sholtz, Charles K.  
REGISTRATION NUMBER: 38,615  
REFERENCE/DOCKET NUMBER: 8600-0152  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 324-0880  
TELEFAX: (415) 324-0960  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 116 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-393-985-16

Query Match 81.9%; Score 181; DB 1; Length 116;  
Best Local Similarity 100.0%; Pred. No. 7.2e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 38  
DB 60 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 94

RESULT 10  
US-08-621-018B-10  
Sequence 10, Application US/08621018B  
Patent No. 6060239  
GENERAL INFORMATION:  
APPLICANT: Stuart, Susan G.  
APPLICANT: Hawkins, Phillip R.  
APPLICANT: Selthamer, Jeffrey J.  
APPLICANT: Murry, Lynn E.  
TITLE OF INVENTION: CELLULREVIN HOMOLOGS  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/621,018B  
FILING DATE: March 22, 1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/409,373  
FILING DATE: March 23, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: GERONE, MICHAEL C.  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PF-0029-1 CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 116 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: GI 433075  
US-08-621-018B-10

Query Match 81.9%; Score 181; DB 3; Length 116;  
Best Local Similarity 100.0%; Pred. No. 7.2e-17;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 38  
DB 60 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 94

Db 60 LSELDPRADALQAGASOFETSAAKLKRYWKNLK 94

RESULT 11

US-08-819-286-2

Sequence 2, Application US/08819286

Patent No. 6169074

GENERAL INFORMATION:

APPLICANT: Montcal, Mauricio

TITLE OF INVENTION: PEPTIDE INHIBITORS OF NEUROTRANSMITTER SECRETION BY NEURONAL CELLS

NUMBER OF SEQUENCES: 29

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 4225 Executive Square, Suite 1400

CITY: La Jolla

STATE: CA

COUNTRY: USA

ZIP: 92037

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/819,286

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 60/013,599

FILING DATE: 18-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: Taylor, Stacy L.

REGISTRATION NUMBER: 34,842

REFERENCE/DOCKET NUMBER: 07349/005001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 619/678-5070

TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 116 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-819-286-2

Query Match 81.9%; Score 181; DB 3; Length 116;

Best Local Similarity 100.0%; Pred. No. 7.2e-17;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 60 LSELDPRADALQAGASOFETSAAKLKRYWKNLK 94

RESULT 12

US-09-483-665-10

Sequence 10, Application US/09483665

Patent No. 6534275

GENERAL INFORMATION:

APPLICANT: Stuart, Susan G.

APPLICANT: Hawkins, Phillip R.

APPLICANT: Selhamer, Jeffrey J.

APPLICANT: Murry, Lynn E.

TITLE OF INVENTION: CELLULREVIN HOMOLOGS

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: U.S.

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/483,665

FILING DATE: Herewith

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/621,018

FILING DATE: March 22, 1996

APPLICATION NUMBER: 08/409,373

FILING DATE: March 23, 1995

ATTORNEY/AGENT INFORMATION:

NAME: Hamlet-Cox, Diana

REGISTRATION NUMBER: 33,302

REFERENCE/DOCKET NUMBER: PF-0029-2 DIV

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-849-8886

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 116 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE:

LIBRARY: GENBANK

CLONE: GI 433075

US-09-483-665-10

Query Match 81.9%; Score 181; DB 4; Length 116;

Best Local Similarity 100.0%; Pred. No. 7.2e-17;

Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 60 LSELDPRADALQAGASOFETSAAKLKRYWKNLK 94

RESULT 13

US-08-621-018B-11

Sequence 11, Application US/08621018B

Patent No. 6060239

GENERAL INFORMATION:

APPLICANT: Stuart, Susan G.

APPLICANT: Hawkins, Phillip R.

APPLICANT: Selhamer, Jeffrey J.

APPLICANT: Murry, Lynn E.

TITLE OF INVENTION: CELLULREVIN HOMOLOGS

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSEE: Incyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: U.S.

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/621,018B

FILING DATE: March 22, 1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/409,373

FILING DATE: March 23, 1995

ATTORNEY/AGENT INFORMATION:

NAME: CERRONE, MICHAEL C.

REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PF-0029-1 CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 82 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: GI 606978  
US-08-621-01B-11

Query Match 81.0%; Score 179; DB 3; Length 82;  
Best Local Similarity 97.1%; Pred. No. 9,1e-17;  
Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 38  
|||||  
26 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 60

Db

RESULT 14  
US-09-483-665-11  
Sequence 11, Application US/09483665  
Patent No. 6534275  
GENERAL INFORMATION:  
APPLICANT: Stuart, Susan G.  
APPLICANT: Hawkins, Phillip R.  
APPLICANT: Seilhammer, Jeffrey J.  
APPLICANT: Murry, Lynn E.  
TITLE OF INVENTION: CELIBREVIN HOMOLOGS  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: Pasteo Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/483,665  
FILING DATE: Herewith  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/621,018  
FILING DATE: March 22, 1996  
APPLICATION NUMBER: 08/409,373  
FILING DATE: March 23, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Hamlet-Cox, Diana  
REGISTRATION NUMBER: 33,302  
REFERENCE/DOCKET NUMBER: PF-0029-2 DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-849-8886  
TELEFAX: 650-849-0555  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 82 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK

CLONE: GI 606978  
US-09-483-665-11

Query Match 81.0%; Score 179; DB 4; Length 82;  
Best Local Similarity 97.1%; Pred. No. 9,1e-17;  
Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 38  
|||||  
26 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 60

Db

RESULT 15  
US-08-760-001-9  
Sequence 9, Application US/08760001  
Patent No. 5962637  
GENERAL INFORMATION:  
APPLICANT: Stone, Clifford C.  
APPLICANT: Hallis, Bassam  
APPLICANT: James, Benjamin A. F.  
APPLICANT: Quinn, Conrad P.  
TITLE OF INVENTION: TOXIN ASSAY  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sterne, Kessler, Goldstein & Fox, P.L.L.C.  
STREET: 1100 New York Ave., N.W., Suite 600  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20005-3934  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/760,001  
FILING DATE: Herewith  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB95/01279  
FILING DATE: 02-JUN-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Esmond, Robert W.  
REGISTRATION NUMBER: 32,893  
REFERENCE/DOCKET NUMBER: 1581.0120001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-371-2600  
TELEFAX: 202-371-2543  
INFORMATION FOR SEQ ID NO: 9:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 35 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
US-08-760-001-9

Query Match 80.1%; Score 177; DB 2; Length 35;  
Best Local Similarity 97.1%; Pred. No. 6,6e-17;  
Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 38  
|||||  
1 LSELDPRADALQAGASQFETSAAKLKRYWKNLK 35

Db

Search completed: November 1, 2004, 18:19:42  
Job time : 29.125 secs



Tue Nov 2 10:45:15 2004

us-10-802-574-9.rapb

Page 1

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: November 1, 2004, 17:59:20 ; Search time 82.875 Seconds  
(without alignments)  
164.308 Million cell updates/sec

Title: US-10-802-574-9

Perfect score: 221  
Sequence: 1 XGGISEIDDPADALQAGASQ.....TSAAKLKRYWKMLKGGGC 42

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1370721 seqs, 324215800 residues

Total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

Result No.	Score	Query Match	Length	DB ID	Description
1	220	99.5	42	10	US-09-962-360B-9
2	181	81.9	116	10	US-09-942-024-4
3	181	81.9	116	10	US-09-942-024-17
4	181	81.9	116	10	US-09-942-024-18
5	181	81.9	116	10	US-09-942-024-18
6	181	81.9	116	10	US-09-942-024-18
7	181	81.9	116	10	US-09-942-024-18
8	181	81.9	116	10	US-09-942-024-18
9	181	81.9	116	10	US-09-942-024-18
10	181	81.9	116	10	US-09-942-024-18
11	181	81.9	116	10	US-09-942-024-18
12	181	81.9	116	10	US-09-942-024-18
13	179	81.0	82	14	US-10-357-028-11

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

14	179	81.0	114	10	US-09-942-024-19	Sequence 19, Appl
15	179	81.0	114	10	US-09-942-024-19	Sequence 19, Appl
16	179	81.0	114	10	US-10-261-161-14	Sequence 14, Appl
17	176	79.6	100	14	US-10-357-028-6	Sequence 6, Appl
18	176	79.6	103	14	US-10-357-028-9	Sequence 9, Appl
19	176	79.6	347	14	US-10-100-957A-28	Sequence 28, Appl
20	176	79.6	350	14	US-10-100-957A-30	Sequence 30, Appl
21	176	79.6	365	10	US-09-223-670-52	Sequence 52, Appl
22	172	77.8	117	16	US-10-467-595-27	Sequence 27, Appl
23	172	77.8	118	10	US-09-942-024-36	Sequence 36, Appl
24	172	77.8	118	10	US-09-942-024-36	Sequence 36, Appl
25	172	77.8	118	10	US-10-261-161-10	Sequence 10, Appl
26	170	76.9	35	10	US-09-962-360B-3	Sequence 3, Appl
27	169	76.5	35	10	US-09-962-360B-3	Sequence 3, Appl
28	161	72.9	40	10	US-09-942-024-58	Sequence 58, Appl
29	161	72.9	40	10	US-09-942-024-60	Sequence 60, Appl
30	161	72.9	40	10	US-09-942-024-61	Sequence 61, Appl
31	161	72.9	40	10	US-09-942-024-61	Sequence 61, Appl
32	161	72.9	40	10	US-09-942-024-61	Sequence 61, Appl
33	161	72.9	40	10	US-09-942-024-61	Sequence 61, Appl
34	161	72.9	40	10	US-10-261-161-83	Sequence 83, Appl
35	161	72.9	40	10	US-10-261-161-83	Sequence 83, Appl
36	161	72.9	40	10	US-10-261-161-85	Sequence 85, Appl
37	159	71.9	109	14	US-10-369-493-6364	Sequence 6364, Ap
38	157	71.0	40	10	US-09-942-024-57	Sequence 57, Appl
39	157	71.0	40	10	US-09-942-024-55	Sequence 55, Appl
40	157	71.0	40	10	US-09-942-024-57	Sequence 57, Appl
41	157	71.0	40	10	US-09-942-024-57	Sequence 57, Appl
42	157	71.0	40	10	US-10-261-161-82	Sequence 82, Appl
43	157	71.0	40	10	US-10-261-161-82	Sequence 82, Appl
44	157	71.0	104	15	US-09-942-024-20	Sequence 20, Appl
45	157	71.0	104	10	US-09-942-024-20	Sequence 20, Appl

#### ALIGNMENTS

```
RESULT 1
US-09-962-360B-9
; Sequence 9, Application US/09962360B
; Publication No. US2003007685A1
; GENERAL INFORMATION:
; /9
; APPLICANT: Schmidt, James J.
; APPLICANT: Stafford, Robert G.
; TITLE OF INVENTION: High Throughput Assays for the Proteolytic Activities of Clostrid:
; TITLE OF INVENTION: Neurotoxins
; FILE REFERENCE: 003/224/SAP
; CURRENT APPLICATION NUMBER: US/09/962,360B
; CURRENT FILING DATE: 2002-08-19
; PRIOR APPLICATION NUMBER: US 60/235,050
; PRIOR FILING DATE: 2001-09-25
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 9
; LENGTH: 42
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide chosen such that it is cleaved by BONT B
; NAME/KEY: misc_feature
; LOCATION: 1
; OTHER INFORMATION: Xaa at 1 is N-fluoresceinyl-glycine
US-09-962-360B-9

Query Match 99.5%; Score 220; DB 10; Length 42;
Best Local Similarity 100.0%; Pred. No. 9.3e-22;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
RESULT 2
US-09-942-024-4
; Sequence 4, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-024-4

Query Match      81.9%; Score 181; DB 10; Length 116;
Best Local Similarity 100.0%; Pred. No. 4e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy
4 LSELDPRADALQAGASQFETSAAKLKRYKWKXK 38
60 LSELDPRADALQAGASQFETSAAKLKRYKWKXK 94

RESULT 3
US-09-942-024-17
; Sequence 17, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-942-024-17

Query Match      81.9%; Score 181; DB 10; Length 116;
Best Local Similarity 100.0%; Pred. No. 4e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy
4 LSELDPRADALQAGASQFETSAAKLKRYKWKXK 38
60 LSELDPRADALQAGASQFETSAAKLKRYKWKXK 94

RESULT 4
US-09-942-024-18
; Sequence 18, Application US/09942024
; Publication No. US20030143650A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
```

```
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Bos taurus
US-09-942-024-18
```

```
Query Match      81.9%; Score 181; DB 10; Length 116;
Best Local Similarity 100.0%; Pred. No. 4e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Cy
4 LSELDPRADALQAGASQFETSAAKLKRYKWKXK 38
60 LSELDPRADALQAGASQFETSAAKLKRYKWKXK 94
```

```
RESULT 5
US-09-942-098-4
; Sequence 4, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-942-098-4
```

```
Query Match      81.9%; Score 181; DB 10; Length 116;
Best Local Similarity 100.0%; Pred. No. 4e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy
4 LSELDPRADALQAGASQFETSAAKLKRYKWKXK 38
60 LSELDPRADALQAGASQFETSAAKLKRYKWKXK 94
```

```
RESULT 6
US-09-942-098-17
; Sequence 17, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Steward, Lance E.
; APPLICANT: Fernandez-Salas, Ester
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 116
; TYPE: PRT
; ORGANISM: Mus musculus
US-09-942-098-17
```

```
Query Match      81.9%; Score 181; DB 10; Length 116;
Best Local Similarity 100.0%; Pred. No. 4e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

QY 4 LSELDPRADALQAGASQFETSAKLRKRYWKNLK 38  
DB 60 LSELDPRADALQAGASQFETSAKLRKRYWKNLK 94

## RESULT 7

US-09-942-098-18  
Sequence 18, Application US/09942098  
Publication No. US20030143651A1  
GENERAL INFORMATION:  
APPLICANT: Steward, Lance E.  
APPLICANT: Fernandez-Salas, Ester  
APPLICANT: Aoki, Kei Roger  
TITLE OF INVENTION: Fret Fluorescence Assays for Clostridial  
TITLE OF INVENTION: Toxins  
FILE REFERENCE: P-AR 4802  
CURRENT APPLICATION NUMBER: US/09/942,098  
CURRENT FILING DATE: 2001-08-28  
NUMBER OF SEQ ID NOS: 96  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 18  
LENGTH: 116  
TYPE: PRT  
ORGANISM: Bos taurus  
US-09-942-098-18

Query Match 81.9%; Score 181; DB 10; Length 116;  
Best Local Similarity 100.0%; Pred. No. 4e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDPRADALQAGASQFETSAKLRKRYWKNLK 38  
DB 60 LSELDPRADALQAGASQFETSAKLRKRYWKNLK 94

## RESULT 8

US-10-357-028-10  
Sequence 10, Application US/10357028  
Publication No. US20030180931A1  
GENERAL INFORMATION:

APPLICANT: Stuart, Susan G.

Hawkins, Phillip R.

Seilhammer, Jeffrey J.

Murphy, Lynn E.

TITLE OF INVENTION: CELLUBREVIN HOMOLOGS

NUMBER OF SEQUENCES: 51

CORRESPONDENCE ADDRESS:

ADDRESSER: Inocyte Pharmaceuticals, Inc.

STREET: 3174 Porter Drive

CITY: Palo Alto

STATE: CA

COUNTRY: U.S.

ZIP: 94304

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

OPERATING SYSTEM: DOS

SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/357,028

FILING DATE: 29-Jan-2003

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/483,665

FILING DATE: Herewith

APPLICATION NUMBER: 08/621,018

FILING DATE: March 22, 1996

APPLICATION NUMBER: 08/409,373

FILING DATE: March 23, 1995

ATTORNEY/AGENT INFORMATION:

NAME: Hamlet-Cox, Diana

REGISTRATION NUMBER: 33,302

REFERENCE/DOCKET NUMBER: PF-0029-2 DIV

## TELECOMMUNICATION INFORMATION:

TELEPHONE: 650-855-0555

TELEFAX: 650-849-8886

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 116 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

IMMEDIATE SOURCE:

LIBRARY: GENBANK

CLONE: GI 433075

SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-10-357-028-10

Query Match 81.9%; Score 181; DB 14; Length 116;  
Best Local Similarity 100.0%; Pred. No. 4e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDPRADALQAGASQFETSAKLRKRYWKNLK 38  
DB 60 LSELDPRADALQAGASQFETSAKLRKRYWKNLK 94

## RESULT 9

US-10-261-161-11

Sequence 11, Application US/10261161

Publication No. US20040072270A1

GENERAL INFORMATION:

APPLICANT: Fernandez-Salas, Ester

APPLICANT: Steward, Lance E.

APPLICANT: Aoki, Kei Roger

TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy

TRANSFER (FRET) Assays for Clostridial Toxins

FILE REFERENCE: P-AR 4804

CURRENT APPLICATION NUMBER: US/10/261,161

CURRENT FILING DATE: 2002-09-27

NUMBER OF SEQ ID NOS: 109

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 11

LENGTH: 116

TYPE: PRT

ORGANISM: Homo sapiens

US-10-261-161-11

Query Match 81.9%; Score 181; DB 15; Length 116;  
Best Local Similarity 100.0%; Pred. No. 4e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDPRADALQAGASQFETSAKLRKRYWKNLK 38  
DB 60 LSELDPRADALQAGASQFETSAKLRKRYWKNLK 94

## RESULT 10

US-10-261-161-12

Sequence 12, Application US/10261161

Publication No. US20040072270A1

GENERAL INFORMATION:

APPLICANT: Fernandez-Salas, Ester

APPLICANT: Steward, Lance E.

APPLICANT: Aoki, Kei Roger

TITLE OF INVENTION: Cell-Based Fluorescence Resonance Energy

TRANSFER (FRET) Assays for Clostridial Toxins

FILE REFERENCE: P-AR 4804

CURRENT APPLICATION NUMBER: US/10/261,161

CURRENT FILING DATE: 2002-09-27

NUMBER OF SEQ ID NOS: 109

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 12

LENGTH: 116

TYPE: PRT

ORGANISM: Mus musculus  
US-10-261-161-12

Query Match 81.9%; Score 181; DB 15; Length 116;  
Best Local Similarity 100.0%; Pred. No. 4e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDPRADALQAGASQFETSAKLKRYWKXNLK 38  
DB 60 LSELDPRADALQAGASQFETSAKLKRYWKXNLK 94

RESULT 11  
US-10-261-161-13

Sequence 13, Application US/10261161  
Publication No. US20040072270A1  
GENERAL INFORMATION:  
APPLICANT: Fernandez-Salas, Ester  
APPLICANT: Steward, Lance E.  
TITLE OF INVENTION: Cell-based Fluorescence Resonance Energy  
Transfer (FRET) Assays For Clostridial Toxins  
FILE REFERENCE: P-R 4804  
CURRENT FILING DATE: 2002-09-27  
NUMBER OF SEQ ID NOS: 109  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 13  
LENGTH: 116  
TYPE: PRT  
ORGANISM: Bos taurus  
US-10-261-161-13

Query Match 81.9%; Score 181; DB 15; Length 116;  
Best Local Similarity 100.0%; Pred. No. 4e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDPRADALQAGASQFETSAKLKRYWKXNLK 38  
DB 60 LSELDPRADALQAGASQFETSAKLKRYWKXNLK 94

RESULT 12  
US-09-293-670-55

Sequence 55, Application US/09293670  
Publication No. US20030190684A1  
GENERAL INFORMATION:  
APPLICANT: Fisher, Joseph  
APPLICANT: Lorens, James  
APPLICANT: Payan, Donald  
APPLICANT: Rossi, Alexander  
TITLE OF INVENTION: Multiparameter Facs Assays to Detect Alterations in  
Title of Invention: Cellular Parameters and to Screen Small Molecule  
File Reference: A68104/DB/RMS/DAV  
CURRENT FILING DATE: 1999-04-16  
NUMBER OF SEQ ID NOS: 57  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO: 55  
LENGTH: 607  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-293-670-55

Query Match 81.9%; Score 181; DB 10; Length 607;  
Best Local Similarity 100.0%; Pred. No. 2.3e-15;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDPRADALQAGASQFETSAKLKRYWKXNLK 38  
DB 60 LSELDPRADALQAGASQFETSAKLKRYWKXNLK 94

DB 61 LSELDPRADALQAGASQFETSAKLKRYWKXNLK 95

RESULT 13  
US-10-357-028-11

Sequence 11, Application US/10357028  
Publication No. US20030180931A1  
GENERAL INFORMATION:  
APPLICANT: Stuart, Susan G.  
APPLICANT: Hawkins, Phillip R.  
APPLICANT: Selkner, Jeffrey J.  
APPLICANT: Murry, Lynn E.  
TITLE OF INVENTION: CELLULREVIN HOMOLOGS  
NUMBER OF SEQUENCES: 51  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: U.S.  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
FILING DATE: 29-Jan-2003  
APPLICATION NUMBER: US/10/357,028  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/09/483,665  
FILING DATE: Herewith  
APPLICATION NUMBER: 08/621,018  
FILING DATE: March 22, 1996  
APPLICATION NUMBER: 08/409,373  
FILING DATE: March 23, 1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Hamlet-Cox, Diana  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: PF-0029-2 DIV  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-849-8886  
TELEFAX: 650-849-8886  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 82 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: GENBANK  
CLONE: GI 606978  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-10-357-028-11

Query Match 81.0%; Score 179; DB 14; Length 82;  
Best Local Similarity 97.1%; Pred. No. 5.1e-16;  
Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDPRADALQAGASQFETSAKLKRYWKXNLK 38  
DB 26 LSELDPRADALQAGASQFETSAKLKRYWKXNLK 60

RESULT 14  
US-09-942-024-19

Sequence 19, Application US/09942024  
Publication No. US20030143650A1  
GENERAL INFORMATION:  
APPLICANT: Steward, Lance E.  
APPLICANT: Fernandez-Salas, Ester  
APPLICANT: Aoki, Kei Roger

```
; TITLE OF INVENTION: Fret Protease Assays For Botulinum
; TITLE OF INVENTION: Serotype A/E Toxins
; FILE REFERENCE: P-AR 4803
; CURRENT APPLICATION NUMBER: US/09/942,024
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-09-942-024-19
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```
Query Match 81.0%; Score 179; DB 10; Length 114;
Best Local Similarity 97.1%; Pred. No. 7.2e-16;
Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 4 LSEIDDRADALQAGASQFETSAKLRKRYWKNLK 38
Db 58 LSEIDDRADALQAGASQFETSAKLRKRYWKNLK 92
```

## RESULT 15

```
US-09-942-098-19
; Sequence 19, Application US/09942098
; Publication No. US20030143651A1
; GENERAL INFORMATION:
; APPLICANT: Steward, Lance E.
; APPLICANT: Aoki, Kei Roger
; TITLE OF INVENTION: Fret Protease Assays For Clostridial
; TITLE OF INVENTION: Toxins
; FILE REFERENCE: P-AR 4802
; CURRENT APPLICATION NUMBER: US/09/942,098
; CURRENT FILING DATE: 2001-08-28
; NUMBER OF SEQ ID NOS: 96
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 19
; LENGTH: 114
; TYPE: PRT
; ORGANISM: Xenopus laevis
US-09-942-098-19
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Query Match 81.0%; Score 179; DB 10; Length 114;
Best Local Similarity 97.1%; Pred. No. 7.2e-16;
Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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OY 4 LSEIDDRADALQAGASQFETSAKLRKRYWKNLK 38
Db 58 LSEIDDRADALQAGASQFETSAKLRKRYWKNLK 92
```

Search completed: November 1, 2004, 18:23:48  
Job time : 83.875 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: November 1, 2004, 17:52:25 ; Search time 21.75 Seconds  
(without alignments)  
185.798 Million cell updates/sec

Title: US-10-802-574-9  
Perfect score: 221  
Sequence: 1 XGSLSEIDPRADALQAGASQ.....TSAAKLKRYWKXKLGKGGC 42

Scoring table: BLASTSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	181	81.9	116	2 B38315	synaptobrevin 2 -
2	181	81.9	116	2 JN0011	synaptobrevin 2 -
3	181	81.9	116	2 B34288	synaptobrevin 2 -
4	176	79.6	103	2 S35077	cellubrevin - rat
5	172	77.8	118	2 S52747	Vamp1 protein - hu
6	172	77.8	118	2 A38315	synaptobrevin 1 -
7	172	77.8	120	2 A32146	vesicle-associated
8	165	74.7	118	2 A34288	vesicle-associated
9	161	72.9	125	2 S40153	synaptobrevin - 10
10	159	71.9	109	2 T33239	synaptobrevin SNB
11	127	57.5	32	2 S35555	vesicle-associated
12	127	57.5	32	2 S35554	vesicle-associated
13	123	55.7	32	2 S35552	synaptobrevin 150f
14	119	53.8	132	2 JCI522	synaptobrevin 150f
15	119	53.8	152	2 JCI521	vesicle-associated
16	116	52.5	32	2 S35553	vesicle-associated
17	113	51.1	145	2 T21318	hypothetical prote
18	92	41.6	223	2 S47654	integral membrane
19	82	37.1	115	2 S62059	synaptobrevin homo
20	75	33.9	121	2 T39073	synaptobrevin homo
21	72	32.6	117	2 S31250	synaptobrevin homo
22	72	32.6	220	2 T00801	probable synaptobr
23	70	31.7	1237	1 GNFF42	HIV-1 retropepin
24	68	30.8	60	2 D44088	homeotic protein H
25	68	30.8	221	2 F84741	probable synaptobr
26	66	29.9	173	2 D86180	hypothetical prote
27	64	29.0	251	2 AD1145	cyclase H15f homol
28	62.5	28.3	515	2 S59811	vacuolar segregati
29	62	28.1	229	2 F86180	hypothetical prote

30	62	28.1	251	2 AD1504	cyclase H15f homol
31	59	26.7	201	2 S64927	probable membrane
32	59	26.7	609	2 AB9500	glutamine-fructose
33	58	26.2	102	2 S47881	G30A5.4 protein -
34	58	26.2	102	2 T24909	hypothetical prote
35	58	26.2	450	2 A97740	hypothetical prote
36	58	26.2	450	2 A71678	probable response
37	57	25.8	210	2 T16595	hypothetical prote
38	57	25.8	226	2 A97774	pepr protein limpo
39	56.5	25.6	588	2 G82118	succinate dehydrog
40	56	25.3	219	2 T04630	synaptobrevin homo
41	56	25.3	240	2 T47589	synaptobrevin-like
42	56	25.3	454	2 A11641	anthranilate synth
43	56	25.3	663	2 H82731	glutaryl-7-ACA acy
44	55	24.9	565	2 S10367	carboxylesterase (
45	55	24.9	788	2 T44262	transducer protein

## ALIGNMENTS

RESULT 1  
B38315  
synaptobrevin 2 - human  
C/Species: Homo sapiens (man)  
C/Date: 14-Jun-1991 #sequence\_revision 14-Jun-1991 #text\_change 09-Jul-2004  
C/Accession: B38315  
J/Archer III, B.T.; Oezcelik, T.; Jahn, R.; Franke, U.; Suedhof, T.C.  
J/ Biol. Chem. 265, 17267-17273, 1990  
A/Title: Structures and chromosomal localizations of two human genes encoding synaptobrev  
A/Reference number: A38315; MUID:91009161; PMID:1976629  
A/Accession: B38315  
A/Status: Preliminary  
A/Molecule type: DNA  
A/Residues: 1-116 <ARC>  
A/Cross-references: UNIPROT:P19065; GB:M36205; GB:J05611; NID:G338630; PIDN:AAA60604.1; )  
C/Genetics:  
A/Gene: GDB:SYB2; VAMP-2  
A/Cross-references: GDB:125293; OMIM:185881  
A/Map position: 17pter-17p12  
C/Superfamily: synaptobrevin  
C/Keywords: membrane trafficking; transmembrane protein

Query Match 81.9%; Score 181; DB 2; Length 116;  
Best Local Similarity 100.0%; Pred.No. 1.9e-16;  
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Cy 4 LSELDDRADALQAGASQFETSAKLRKYWKXKLG 38  
Db 60 LSELDDRADALQAGASQFETSAKLRKYWKXKLG 94  
RESULT 2  
JN0011  
synaptobrevin 2 - bovine  
N/Alternate names: SNAP receptor  
C/Species: Bos primigenius tauros (cattle)  
C/Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 09-Jul-2004  
C/Accession: JN0011; S36811; S32363  
C/Suedhof, T.C.; Baumeister, W.; Perin, M.S.; Jahn, R.  
Neuron 2, 1475-1481, 1989  
A/Title: A synaptic vesicle membrane protein is conserved from mammals to Drosophila.  
A/Reference number: A93413; MUID:90180466; PMID:2560644  
A/Accession: JN0011  
A/Molecule type: mRNA  
A/Residues: 1-116 <SUB>  
A/Cross-references: UNIPROT:P19065; GB:X76199; NID:G433075; PIDN:CAA53792.1; PID:G433076  
A/Experimental source: brain  
R/Horiikawa, H.P.M.; Saisu, H.; Ishizuka, T.; Sakine, Y.; Tsugita, A.; Odani, S.; Abe, T.  
FEBS Lett. 330, 236-240, 1993  
A/Title: A complex of rab3A, SNAP-25, VAMP/synaptobrevin-2 and syntaxins in brain presyn  
A/Reference number: S36811; MUID:93374072; PMID:8365494  
A/Accession: S36811





vesicle-associated membrane protein 1 - Pacific electric ray  
 C/Species: Torpedo californica (Pacific electric ray)  
 C/Date: 21-May-1990 #sequence\_revision 21-May-1990 #text\_change 09-Jul-2004  
 C/Accession: A32146  
 R/Tribble, W.S.; Cowan, D.W.; Scheller, R.H.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 4538-4542, 1988  
 A/Title: VAMP-1: a synaptic vesicle-associated integral membrane protein.  
 A/Reference number: A32146; PMID:88248054; PMID:3380805  
 A/Accession: A32146  
 A/Molecule type: mRNA  
 A/Residues: 1-120 <TRI>  
 A/Cross-references: UNIPROT:P13701; EMBL:J03777; NID:G213245; PIDN:AAA9286.1; PID:G2132  
 C/Superfamily: synaptobrevin  
 C/Keywords: membrane protein

Query Match 77.8%; Score 172; DB 2; Length 120;  
 Best Local Similarity 94.3%; Pred. No. 3e-15; Mismatches 1; Indels 0; Gaps 0;  
 Matches 33; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 LSELDLRADALQAGASQFETSAAKLKRYWKNLK 38  
 |||||  
 DB 64 LSELDLRADALQAGASQFETSAAKLKRYWKNLK 98

## RESULT 8

A34288  
 vesicle-associated membrane protein 1 - rat  
 C/Species: Rattus norvegicus (Norway rat)  
 C/Date: 01-Jun-1990 #sequence\_revision 01-Jun-1990 #text\_change 09-Jul-2004  
 C/Accession: A34288  
 R/Eiferink, L.A.; Trimble, W.S.; Scheller, R.H.  
 J. Biol. Chem. 264, 11061-11064, 1989  
 A/Title: Two vesicle-associated membrane protein genes are differentially expressed in v  
 A/Reference number: A34288; PMID:89291844; PMID:2472388  
 A/Accession: A34288  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-118 <EUF>  
 A/Cross-references: UNIPROT:Q63666; GB:M24104; GB:U04827; NID:G207628; PIDN:AAA2322.1;  
 C/Superfamily: synaptobrevin  
 C/Keywords: membrane protein

Query Match 74.7%; Score 165; DB 2; Length 118;  
 Best Local Similarity 91.4%; Pred. No. 2.4e-14; Mismatches 2; Indels 0; Gaps 0;  
 Matches 32; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 LSELDLRADALQAGASQFETSAAKLKRYWKNLK 38  
 |||||  
 DB 62 LSELDLRADALQAGASQFETSAAKLKRYWKNLK 96

## RESULT 9

S40153  
 synaptobrevin - longfin squid  
 C/Species: Loligo pealeii (longfin squid)  
 C/Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 09-Jul-2004  
 C/Accession: S40153  
 R/Bowmer, K.; Kistner, A.; Hasemann, E.; Betz, H.  
 Submitted to the EMBL Data Library, August 1993  
 A/Description: Conservation of primary structure and clostridial neurotoxin cleavage sit  
 A/Reference number: S40153  
 A/Accession: S40153  
 A/Status: preliminary  
 A/Molecule type: mRNA  
 A/Residues: 1-125 <BOW>  
 A/Cross-references: UNIPROT:P47194; EMBL:X74748; NID:G437855; PIDN:CAA2766.1; PID:G4378  
 C/Superfamily: synaptobrevin

Query Match 72.9%; Score 161; DB 2; Length 125;  
 Best Local Similarity 85.7%; Pred. No. 8.6e-14; Mismatches 3; Indels 0; Gaps 0;  
 Matches 30; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 LSELDLRADALQAGASQFETSAAKLKRYWKNLK 38

DB :|||||  
 69 LSELDLRADALQAGASQFETSAAKLKRYWKNLK 103

## RESULT 10

T33239  
 synaptobrevin SNB-1 - Caenorhabditis elegans  
 C/Species: Caenorhabditis elegans  
 C/Date: 29-Oct-1999 #sequence\_revision 29-Oct-1999 #text\_change 09-Jul-2004  
 C/Accession: T33239  
 R/Greco, T.; Bradshaw, H.; O'Brien, D.  
 Submitted to the EMBL Data Library, May 1998  
 A/Description: The sequence of C. elegans cosmid T10H9.  
 A/Reference number: Z21306  
 A/Accession: T33239  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-109 <GRE>  
 A/Cross-references: UNIPROT:Q02495; EMBL:AF067948; PIDN:AACT9234.1; GSPDB:GN00023; CESP:  
 A/Experimental source: strain Bristol N2; clone T10H9  
 C/Genetics:  
 A/Gene: SNB-1; CESP:T10H9.4  
 A/Map position: 5  
 A/Intons: 39/3  
 C/Superfamily: synaptobrevin

Query Match 71.9%; Score 159; DB 2; Length 109;  
 Best Local Similarity 85.7%; Pred. No. 1.4e-13; Mismatches 3; Indels 0; Gaps 0;  
 Matches 30; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 LSELDLRADALQAGASQFETSAAKLKRYWKNLK 38  
 |||||  
 DB 52 LSELDLRADALQAGASQFETSAAKLKRYWKNLK 86

## RESULT 11

S35555  
 vesicle-associated membrane protein 2 - chicken (fragment)  
 C/Species: Gallus gallus (chicken)  
 C/Date: 10-Dec-1993 #sequence\_revision 26-Jul-1996 #text\_change 09-Jul-2004  
 C/Accession: S35555  
 R/Paternello, T.; Bargelloni, L.; Rossetto, O.; Schiavo, G.; Montecucco, C.  
 Nature 364, 581-582, 1993  
 A/Title: Neurotransmission and secretion.  
 A/Reference number: S35552; PMID:93354436; PMID:8350916  
 A/Accession: S35555  
 A/Status: preliminary  
 A/Molecule type: DNA  
 A/Residues: 1-32 <PAT>  
 A/Cross-references: UNIPROT:Q7L264  
 C/Superfamily: synaptobrevin  
 C/Keywords: membrane trafficking; transmembrane protein

Query Match 57.5%; Score 127; DB 2; Length 32;  
 Best Local Similarity 100.0%; Pred. No. 5.8e-10; Mismatches 0; Indels 0; Gaps 0;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDLRADALQAGASQFETSAAKLK 30  
 |||||  
 DB 6 LSELDLRADALQAGASQFETSAAKLK 32

## RESULT 12

S35554  
 vesicle-associated membrane protein 2 - mouse (fragment)  
 C/Species: Mus musculus (house mouse)  
 C/Date: 10-Dec-1993 #sequence\_revision 27-Feb-1997 #text\_change 09-Jul-2004  
 C/Accession: S35554  
 R/Paternello, T.; Bargelloni, L.; Rossetto, O.; Schiavo, G.; Montecucco, C.  
 Nature 364, 581-582, 1993  
 A/Title: Neurotransmission and secretion.  
 A/Reference number: S35552; PMID:93354436; PMID:8350916  
 A/Accession: S35554  
 A/Status: preliminary

A:Molecule type: DNA  
A:Residues: 1-32 <PAT>  
A:Cross-references: UNIPROT:035619  
C:Superfamily: synaptoobrevin

Query Match 57.5%; Score 127; DB 2; Length 32;  
Best local similarity 100.0%; Pred. No. 5.8e-10;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LSELDDRADALQAGASQFETSAKTKR 30  
Db 6 LSELDDRADALQAGASQFETSAKTKR 32

## RESULT 13

335552  
vesicle-associated membrane protein 1 - mouse (fragment)  
C:Species: Mus musculus (house mouse)  
C>Date: 10-Dec-1993 #sequence\_revision 27-Feb-1997 #text\_change 09-Jul-2004  
C:Accession: S33552  
R:Patarnello, T.; Bargelloni, L.; Rossetto, O.; Schiavo, G.; Montecucco, C.  
Nature 364, 581-582, 1993  
A:Title: Neurotransmission and secretion.  
A:Reference number: S33552, PMID:93354436; PMID:8350916  
A:Accession: S33552  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-32 <PAT>  
A:Cross-references: UNIPROT:Q9CXX2  
C:Superfamily: synaptoobrevin

Query Match 55.7%; Score 123; DB 2; Length 32;  
Best local similarity 96.3%; Pred. No. 1.9e-09;  
Matches 26; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 4 LSELDDRADALQAGASQFETSAKTKR 30  
Db 6 LSELDDRADALQAGASQFETSAKTKR 32

## RESULT 14

JC1522  
synaptoobrevin isoform B - fruit fly (Drosophila melanogaster)  
N:Alternate names: vesicle-associated membrane protein B  
C:Species: Drosophila melanogaster  
C>Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 09-Jul-2004  
C:Accession: JC1522  
R:Chin, A.C.; Burgess, R.W.; Wong, B.R.; Schwarz, T.L.; Scheller, R.H.  
Gene 131, 175-181, 1993  
A:Title: Differential expression of transcripts from syb, a Drosophila melanogaster gene  
A:Reference number: JC1521; PMID:94010306; PMID:8406010  
A:Accession: JC1522  
A:Molecule type: DNA  
A:Residues: 1-132 <CHI>  
A:Cross-references: UNIPROT:P18489; GB:U14270; NID:G290281; PDB:AAA28924.1; PID:G290282  
A:Note: the authors translated the codon AAG for residue 101 as Asn and CGC for residue  
C:Comment: Gene syb comprises five exons. Splicing exons 1.2.3.4.5 results in synaptoobrevin  
C:Genetics:  
A:Gene: syb  
A:Cross-references: FlyBase:FBgn0003660  
A:introns: 16/2; 128/1  
C:Superfamily: synaptoobrevin  
C:Keywords: membrane protein; synaptic vesicle

Query Match 53.8%; Score 119; DB 2; Length 132;  
Best local similarity 65.7%; Pred. No. 2.8e-08;  
Matches 23; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 4 LSELDDRADALQAGASQFETSAKTKRYWKXK 38  
Db 76 LSELGERADOLEGASQSEQAGKTKRKQWYWK 110

## RESULT 15

JC1521  
synaptoobrevin isoform A - fruit fly (Drosophila melanogaster)  
N:Alternate names: vesicle-associated membrane protein A  
C:Species: Drosophila melanogaster  
C>Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 09-Jul-2004  
C:Accession: JC1521; UN0012  
R:Chin, A.C.; Burgess, R.W.; Wong, B.R.; Schwarz, T.L.; Scheller, R.H.  
Gene 131, 175-181, 1993  
A:Title: Differential expression of transcripts from syb, a Drosophila melanogaster gene  
A:Reference number: JC1521; PMID:94010306; PMID:8406010  
A:Accession: JC1521  
A:Molecule type: DNA  
A:Residues: 1-152 <CHI>  
A:Cross-references: UNIPROT:P18489; GB:U14270; NID:G290281; PDB:AAA28924.1; PID:G290283  
A:Note: the authors translated the codon AAG for residue 101 as Asn and CGC for residue  
R:Suedhof, T.C.; Baumeister, M.; Perin, M.S.; Kahn, R.  
Neuron 2, 1475-1481, 1989  
A:Title: A synaptic vesicle membrane protein is conserved from mammals to Drosophila.  
A:Reference number: A93413; PMID:90180466; PMID:2560644  
A:Accession: UN0012  
A:Molecule type: mRNA  
A:Residues: 1-92, 94-152 <SUE>  
C:Comment: Gene syb comprises five exons. Splicing exons 1.2.3.4.5 results in synaptoobrevin  
C:Genetics:  
A:Gene: syb  
A:Cross-references: FlyBase:FBgn0003660  
A:introns: 16/2; 128/1  
C:Superfamily: synaptoobrevin  
C:Keywords: synaptic vesicle; transmembrane protein  
F:111-130/Domain: transmembrane #status predicted <TM>

Query Match 53.8%; Score 119; DB 2; Length 152;  
Best local similarity 65.7%; Pred. No. 3.3e-08;  
Matches 23; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

Qy 4 LSELDDRADALQAGASQFETSAKTKRYWKXK 38  
Db 76 LSELGERADOLEGASQSEQAGKTKRKQWYWK 110

Search completed: November 1, 2004, 17:53:52  
Job time : 21.75 secs



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OX NCB1_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusika K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,
RA Stumpflen M.J., Udell T.B., Tohivuki S., Carninci P., Miliady S.J.,
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Miliady S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.U., Malek J.A., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC061396; AAH61396.1; -
DR InterPro; IPR001388; SynaptoDreVin.
DR Pfam; PF00957; SynaptoDreVin; 1.
DR PRINTS; PR00219; SYNAPTOBREVN.
DR PRODOM; PD001229; SynaptoDreVin; 1.
DR PROSITE; PS00417; SYNAPTOBREVN; 1.
DR PROSITE; PS50892; V_SNAKE; 1.
KW Hypothetical protein.
SQ SEQUENCE 114 AA; 12440 MW; 0EE3EADBDP2A1ABE CRC64;

Query Match 81.9%; Score 181; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 7.7e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDPRADALQAGASQFETSAKTKRKYWKXK 38
DB 58 LSELDPRADALQAGASQFETSAKTKRKYWKXK 92

RESULT 3
AAH61396 PRELIMINARY; PRT; 114 AA.
AC AAH61396;
DT 25-MAR-2004 (TrEMBLrel. 27, Created)
DT 25-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT 25-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein MG073977.
GN MG073977.
OS Xenopus tropicalis (western clawed frog) (Silurana tropicalis).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodidae; Xenopus; Silurana.
CX NCB1_TaxID=8364;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusika K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,
RA Stumpflen M.J., Udell T.B., Tohivuki S., Carninci P., Miliady S.J.,
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Miliady S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.U., Malek J.A., Gay L.J., Hulyk S.W.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC061396; AAH61396.1; -
KW Hypothetical protein.
SQ SEQUENCE 114 AA; 12440 MW; 0EE3EADBDP2A1ABE CRC64;

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RA Brownstein M.J., Udell T.B., Tohivuki S., Carninci P., Prange C.,
RA Raha S.S., Loguclano N.A., Peters G.J., Abramson R.D., Miliady S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.U., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RA Klein S., Strausberg R.;
RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC061396; AAH61396.1; -
KW Hypothetical protein.
SQ SEQUENCE 114 AA; 12440 MW; 0EE3EADBDP2A1ABE CRC64;

Query Match 81.9%; Score 181; DB 2; Length 114;
Best Local Similarity 100.0%; Pred. No. 7.7e-16;
Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDPRADALQAGASQFETSAKTKRKYWKXK 38
DB 58 LSELDPRADALQAGASQFETSAKTKRKYWKXK 92

RESULT 4
VAMP2 HUMAN STANDARD; PRT; 115 AA.
ID VAMP2 HUMAN
AC P19065;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Vesicle-associated membrane protein 2 (VAMP-2) (SynaptoDreVin 2).
GN Name=VAMP2; Synonyms=SYB2;
OS Homo sapiens (Human); and
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
CX NCB1_TaxID=9606, 9913;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Human;
RX MEDLINE=91009161; PubMed=1976629;
RA Archer B.T., III, Ozercelek T., Jahn R., Francke U., Suedhof T.C.;
RT "Structures and chromosomal localizations of two human genes encoding
RT synaptoDreVin 1 and 2."
RT J. Biol. Chem. 265:17267-17273 (1990).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Human; TISSUE=Peripheral blood;
RA Nabokina S.M., Iazo P.A., Mollinedo F.;
RT "Expression of VAMP genes in human neutrophils."
RT Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC SPECIES=Human; TISSUE=Blood;
RA Tarsicio D., Zoraghi K.G., Falbo V.;
RT "Genomic structure of human SYB2 gene."
RT Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC SPECIES=Bovine;
RX MEDLINE=90180466; PubMed=2560644;
RA Suedhof T.C., Baumeister M., Perin M.S., Jahn R.;
RT "A synaptic vesicle membrane protein is conserved from mammals to
RT Drosophila."

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RL Neuron 2:1475-1481(1989).  
 RN  
 RN [5] SEQUENCE OF 31-59 AND 67-82, AND ACETYLATION.  
 RP SPECIES=Bovine;  
 RC MEDLINE=93205116; PubMed=8455717;  
 RX MEDLINE=93205116; PubMed=8455717;  
 RA Seiler T., Whiteheart S.W., Brunner M., Erdjument-Bromage H.,  
 RT Geromanos S., Tempst P., Rothman J.E.;  
 RL "SNAP receptors implicated in vesicle targeting and fusion.";   
 Nature 362:318-324(1993).  
 RN  
 RN [6] TISSUE SPECIFICITY.  
 RP SPECIES=Human;  
 RC MEDLINE=96332494; PubMed=8760387;  
 RX Jengdsh M.N., Fernandez C.S., Hewitt D.R., Macaulay S.L., Gough K.H.,  
 RA Grubisov J., Verkuylen A., Cosgrove L., Alafaci A., Frenkel M.J.,  
 RT Ward C.W.;  
 RL "Insulin-responsive tissues contain the core complex protein SNAP-25  
 (synaptosomal-associated protein 25) A and B isoforms in addition to  
 syntaxin 4 and synaptobrevins 1 and 2.";  
 Biochem. J. 317:945-954(1996).  
 RN  
 RN [7] TOPOLOGY.  
 RP SPECIES=Human;  
 RC MEDLINE=95137000; PubMed=7835332;  
 RX Kutay U., Ahnert-Hilger G., Hartmann E., Wiedenmann B., Rapoport T.A.;  
 RA "Transport route for synaptobrevin via a novel pathway of insertion  
 into the endoplasmic reticulum membrane.";  
 EMBO J. 14:217-223(1995).  
 RN  
 RN [8] X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 33-88 IN COMPLEX WITH BOTB.  
 RP SPECIES=Human;  
 RC MEDLINE=20392548; PubMed=10932255; DOI=10.1038/77997;  
 RX Hanson M.A., Stevens R.C.;  
 RA "Crystall structure of synaptobrevin-II bound to botulinum neurotoxin  
 type B at 2.0 A resolution.";  
 Nat. Struct. Biol. 7:687-692(2000).  
 RL  
 RL [1] FUNCTION: Involved in the targeting and/or fusion of transport  
 vesicles to their target membrane.  
 CC [1] SUBUNIT: Interacts with VAMP and VAMPB.  
 CC [1] SUBCELLULAR LOCATION: Type IV membrane protein. Neuronal synaptic  
 vesicles.  
 CC [1] TISSUE SPECIFICITY: Nervous system and skeletal muscle.  
 CC [1] SIMILARITY: Belongs to the synaptobrevin family.  
 CC [1] SIMILARITY: Contains 1 v-SNARE coiled-coil homology domain.  
 CC  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL: M36205; AAA60604.1; -;  
 DR EMBL: M36201; AAA60604.1; JOINED.  
 DR EMBL: M36202; AAA60604.1; JOINED.  
 DR EMBL: M36203; AAA60604.1; JOINED.  
 DR EMBL: M36204; AAA60604.1; JOINED.  
 DR EMBL: AJ225044; CA12385.1; -;  
 DR EMBL: AF135372; AAF15551.1; -;  
 DR EMBL: X76199; CAA53792.1; -;  
 DR PIR: B38315; B38315.  
 DR PIR: JN0011; JN0011.  
 DR PDB: 1F83; X-ray; B=52-75, C=76-87.  
 DR Genew; HGNC:12643; VAMP2.  
 DR MIM; 185881; -;  
 DR GO; GO:0005887; C:integral to plasma membrane; TAS.  
 DR InterPro; IPR001388; Synaptobrevin.  
 DR Pfam; PF00957; Synaptobrevin.1.  
 DR PRINTS; PR00219; SYNAPTOBREVIN.  
 DR Prodom; PD001229; Synaptobrevin.1.  
 DR PROSITE; PS00417; SYNAPTOBREVIN.1.  
 DR PROSITE; PS50892; V\_SNARE.1.

KM 3D-structure; Acetylation; Coiled coil; Direct protein sequencing;  
 KW Multigene family; Synapse; Synaptosome; Transmembrane.  
 FT INIT MET 1 93 Cytoplasmic (Potential).  
 FT DOMAIN 0 0 Anchor for type IV membrane protein  
 FT TRANSMEM 94 113 (Potential).  
 FT DOMAIN 114 115 Vesicular (Potential).  
 FT MOD RES 1 1 N-acetylserine.  
 FT DOMAIN 30 90 v-SNARE coiled-coil homology.  
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 Best Local Similarity 100.0%; Pred. No. 7.8e-16;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 LSELDPRADALQAGASQFETSAKXKRYKWKNLK 38  
 DB 59 LSELDPRADALQAGASQFETSAKXKRYKWKNLK 93  
 RESULT 5  
 VAM2 MOUSE STANDARD; PRT; 115 AA.  
 ID VAM2 MOUSE  
 AC 064357;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-OCT-2004 (Rel. 45, Last annotation update)  
 DE Vesicle-associated membrane protein 2 (VAMP-2) (Synaptobrevin 2).  
 GN Name=Vamp2; Synonyms=Syb2;  
 OS Mus musculus (Mouse); and  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090, 10116;  
 RN [1] SEQUENCE FROM N.A.  
 RP SPECIES=Human;  
 RC MEDLINE=89291844; PubMed=2472368;  
 RX Elferink L.A., Trimble W.S., Scheller R.H.;  
 RA "Two vesicle-associated membrane protein genes are differentially  
 expressed in the rat central nervous system.";  
 J. Biol. Chem. 264:11061-11064(1989).  
 RL  
 RN [2] SEQUENCE FROM N.A.  
 RP SPECIES=Mouse;  
 RC MEDLINE=86104125; PubMed=9430681;  
 RX Martin L.B., Shewan A., Miller C.A., Gould G.W., James D.E.;  
 RA "Vesicle-associated membrane protein 2 plays a specific role in the  
 insulin-dependent trafficking of the facilitative glucose transporter  
 GLUT4 in 3T3-L1 adipocytes.";  
 J. Biol. Chem. 273:1444-1452(1998).  
 RL  
 RN [3] X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 1-96 IN COMPLEX WITH STX1A  
 RP AND SNAP25.  
 RP SPECIES=Rat;  
 RC MEDLINE=98430524; PubMed=9759724; DOI=10.1038/26412;  
 RX Sutton R.B., Faehauer D., Jahn R., Brunger A.T.;  
 RA "Crystal structure of a SNARE complex involved in synaptic exocytosis  
 at 2.4 A resolution.";  
 Nature 395:347-353(1998).  
 RN  
 RN [4] X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 29-93 IN COMPLEX WITH STX1A;  
 RP CPLX1 AND SNAP25.  
 RP SPECIES=Rat;  
 RC MEDLINE=21822661; PubMed=11832227;  
 RX Chen X., Tomchick D.R., Kovriggin E., Arac D., Machius M.,  
 RA Suedhof T.C., Rizo J.;  
 RA "Three-dimensional structure of the complexin/SNARE complex.";  
 Neuron 33:397-409(2002).  
 RL  
 RN [5] X-RAY CRYSTALLOGRAPHY (1.45 ANGSTROMS) OF 28-89 IN COMPLEX WITH STX1A  
 RP AND SNAP25.  
 RP SPECIES=Rat;

RX MEDLINE=2249607; PubMed=12496247; DOI=10.1074/jbc.M211899200;  
 RA Ernst J.A., Brunker A.T.;  
 RT "High resolution structure, stability, and synaptobrevin binding of a  
 RL truncated neuronal SNARE complex";  
 CC J. Biol. Chem. 278:8630-8636(2003).  
 CC -1- FUNCTION: Involved in the targeting and/or fusion of transport  
 CC vesicles to their target membrane.  
 CC -1- SUBUNIT: Interacts with VAMP and VAPB (By similarity). Part of the  
 CC SNARE core complex containing SNAP25, VAMP2 and STX1A. This  
 CC complex binds to CGLX1.  
 CC -1- SUBCELLULAR LOCATION: Type IV membrane protein. Neuronal synaptic  
 CC vesicles.  
 CC -1- TISSUE SPECIFICITY: Nervous system specific. A higher level  
 CC expression is seen in the brain as compared to the spinal cord.  
 CC -1- SIMILARITY: Belongs to the synaptobrevin family.  
 CC -1- SIMILARITY: Contains 1 V-SNARE coiled-coil homology domain.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: M24105; AAA3321.1; -;  
 DR EMBL: U60150; AA03463.1; -;  
 DR PIR: B34288; B34288.  
 DR PDB: 1KIL; X-ray; A=26-91.  
 DR PDB: 1N7S; X-ray; A=26-88.  
 DR PDB: 1SPC; X-ray; A/E/I=1-95.  
 DR MGD: MGI:131327; Vamp2.  
 DR RGD: 3949; Vamp2.  
 DR InterPro: IPR001388; Synaptobrevin.  
 DR Pfam: PF00957; Synaptobrevin.1.  
 DR PRINTS: PR00219; SYNAPTOBREVN.  
 DR ProDom: PD001229; Synaptobrevin.1.  
 DR PROSITE: PS00417; SYNAPTOBREVN; 1.  
 DR PROSITE: PS50892; V-SNARE; 1.  
 DR 3D-structure: Acetylation: Coiled coil; Multigene family;  
 KM Polymerism: Synapse; Synaposome; Transmembrane.  
 FT INT MET 0 By similarity.  
 FT DOMAIN 1 93 Cytoplasmic (Potential).  
 FT TRANSMEM 94 113 Anchor for type IV membrane protein  
 FT (Potential).  
 FT DOMAIN 114 115 Vesicular (Potential).  
 FT MOD RS 1 1 N-acetylseryl (By similarity).  
 FT DOMAIN 30 90 V-SNARE coiled-coil homology.  
 FT VARIANT 110 110 I -> I.  
 FT VARIANT 111 111 V -> I.  
 FT HELIX 28 87  
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 Query Match 81.9%; Score 181; DB 1; Length 115;  
 Best Local Similarity 100.0%; Pred. No. 7.8e-16;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 59 LSELDPRADALQAGASQFETSAKTKRKYWKXK 38  
 4 LSELDPRADALQAGASQFETSAKTKRKYWKXK 38  
 59 LSELDPRADALQAGASQFETSAKTKRKYWKXK 93  
 RESULT 6  
 ID Q9BUC2 PRELIMINARY; PRT; 116 AA.  
 AC Q9BUC2;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-OCT-2004 (TrEMBLrel. 28, Last annotation update)  
 DE Vesicle-associated membrane protein 2 (Synaptobrevin 2).  
 OS Name=VAMP2;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC MEDLINE=2238657; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diachenko L., Marusik A., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein W.J., Ustin T.B., Toshitsuki S., Canninci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,  
 RA Richards S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Hellon E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalski U., Smallos D.E., Scherch A., Schein J.E.,  
 RA Jones S.J., Marz M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Testis;  
 RA Strausberg R.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Lung;  
 RA Strausberg R.;  
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC002737; AA02737.3; -;  
 DR EMBL: BC019608; AA019608.1; -;  
 DR EMBL: BC033870; AA033870.1; -;  
 DR HSSP: Q9WUM2; 1SFC.  
 DR InterPro: IPR001388; Synaptobrevin.  
 DR Pfam: PF00957; Synaptobrevin.1.  
 DR PRINTS: PR00219; SYNAPTOBREVN.  
 DR ProDom: PD001229; Synaptobrevin.1.  
 DR PROSITE: PS00417; SYNAPTOBREVN; 1.  
 DR PROSITE: PS50892; V-SNARE; 1.  
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 Best Local Similarity 100.0%; Pred. No. 7.8e-16;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Db 60 LSELDPRADALQAGASQFETSAKTKRKYWKXK 94  
 4 LSELDPRADALQAGASQFETSAKTKRKYWKXK 38  
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 AC Q9NOY0;  
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 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE VAMP-2.  
 OS Macaca mulatta (Rhesus macaque).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;

CC Cercopithecinae; Macaca.  
 OX NCBI\_TaxID=9544;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Hippocampus;  
 RA Jensen M.J., Smith L.A.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF240769; AAF64476.1; -  
 DR HSSP; Q9WTW2; 1SFC.  
 DR InterPro; IPR001388; Synaptoobrevin.  
 DR Pfam; PF00957; Synaptoobrevin.1.  
 DR PRINTS; PR00219; SYNAPTOBREVN.  
 DR ProDom; PD001229; synaptoobrevin; 1.  
 DR PROSITE; PS00417; SYNAPTOBREVN; 1.  
 DR PROSITE; PS50892; V\_SNAKE; 1.  
 SQ SEQUENCE 116 AA; 12663 MW; 9CD679C4F6F1B5A8 CRC64;

Query Match 81.9%; Score 181; DB 2; Length 116;  
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Oy 4 LSELDPRADALQAGASQFETSAKLRKRYWKNLK 38  
 Db 60 LSELDPRADALQAGASQFETSAKLRKRYWKNLK 94

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 DT 01-JAN-1998 (TREMblrel. 05; Created)  
 DT 01-JAN-1998 (TREMblrel. 05; Last sequence update)  
 DT 01-MAR-2004 (TREMblrel. 26; Last annotation update)  
 DE Vesicle associated membrane protein 2.  
 GN Name=Vamp2; Synonyms=wtVAMP-2;  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Olsen S.K., Doerre S., Corley R.B.;  
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AF007168; AAB62931.1; -  
 DR PIR; S3554; S3554.  
 DR HSSP; Q9WTW2; 1SFC.  
 DR MGD; MGI:131277; Vamp2.  
 DR GO; GO:0030141; C:secretory granule; IDA.  
 DR GO; GO:0030672; C:synaptic vesicle membrane; IDA.  
 DR GO; GO:0042589; C:zymogen granule membrane; IDA.  
 DR GO; GO:0005516; P:calmodulin binding; IDA.  
 DR GO; GO:0005543; P:phospholipid binding; IDA.  
 DR GO; GO:0000149; F:SNARE binding; IDA.  
 DR GO; GO:0017156; P:calcium ion-dependent exocytosis; IDA.  
 DR GO; GO:0017157; P:regulation of exocytosis; IDA.  
 DR GO; GO:0016083; P:synaptic vesicle fusion; IMP.  
 DR InterPro; IPR001388; Synaptoobrevin.  
 DR Pfam; PF00957; Synaptoobrevin.1.  
 DR PRINTS; PR00219; SYNAPTOBREVN.  
 DR ProDom; PD001229; synaptoobrevin; 1.  
 DR PROSITE; PS00417; SYNAPTOBREVN; 1.  
 DR PROSITE; PS50892; V\_SNAKE; 1.  
 SQ SEQUENCE 116 AA; 12677 MW; 4E1DD0D56B5409D0A CRC64;

Query Match 81.9%; Score 181; DB 2; Length 116;  
 Best Local Similarity 100.0%; Pred. No. 7.8e-16;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 LSELDPRADALQAGASQFETSAKLRKRYWKNLK 38  
 Db 60 LSELDPRADALQAGASQFETSAKLRKRYWKNLK 94

RESULT 9  
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 ID AAH02737 PRELIMINARY; PRT; 116 AA.  
 AC AAH02737;  
 DT 14-APR-2004 (TREMblrel. 27; Created)  
 DT 14-APR-2004 (TREMblrel. 27; Last sequence update)  
 DT 14-APR-2004 (TREMblrel. 27; Last annotation update)  
 DE Vesicle-associated membrane protein 2 (Synaptoobrevin 2).  
 GN VAMP2.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Vax S.I., Wang U., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaney S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.U., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalish D.E., Scherch A., Schein J.E.,  
 RA Jones S.U., Matra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RA Strausberg R.;  
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC002737; AAH02737.3; -  
 SQ SEQUENCE 116 AA; 12663 MW; 9CD679C4F6F1B5A8 CRC64;

Query Match 81.9%; Score 181; DB 2; Length 116;  
 Best Local Similarity 100.0%; Pred. No. 7.8e-16;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 LSELDPRADALQAGASQFETSAKLRKRYWKNLK 38  
 Db 60 LSELDPRADALQAGASQFETSAKLRKRYWKNLK 94

RESULT 10  
 AAH55105  
 ID AAH55105 PRELIMINARY; PRT; 116 AA.  
 AC AAH55105;  
 DT 14-APR-2004 (TREMblrel. 27; Created)  
 DT 14-APR-2004 (TREMblrel. 27; Last sequence update)  
 DT 14-APR-2004 (TREMblrel. 27; Last annotation update)  
 DE Vesicle-associated membrane protein 2.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,



RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko U., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo W.F., Caesavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Franke C.,  
 RA Raba S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gnatratne P.H.,  
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalon D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy U., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting U., Madan A., Young A.C., Shevchenko Y., Souffard G.O.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywnicki M.I., Skalska U., Smalhus D.S., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]  
 SEQUENCE FROM N.A.

RC TISSUE=Brain;  
 RA Strausberg R.;

RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL: BC055105; AAH5105.1; - 4A0D0D56B5409D0A CRC64;

SQ SEQUENCE 116 AA; 12691 MW; 4A0D0D56B5409D0A CRC64;

Query Match 81.9%; Score 181; DB 2; Length 116;  
 Best Local Similarity 100.0%; Pred. No. 7.8e-16;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 LSELDDRADALQAGASOFETSAAKLRKRYWKXK 38  
 60 LSELDDRADALQAGASOFETSAAKLRKRYWKXK 94

RESULT 11  
 BAC41125 PRELIMINARY; PRT; 116 AA.

AC BAC41125;  
 DT 14-APR-2004 (TREMBLrel. 27, Created)

DT 14-APR-2004 (TREMBLrel. 27, Last sequence update)

DT 14-APR-2004 (TREMBLrel. 27, Last annotation update)

DE 15 days embryo brain cDNA, RIKEN full-length enriched library,  
 DE clone:G660012G02 product:unclassified, full insert sequence.

OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;  
 [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Brain;  
 RX MEDLINE=22354683; PubMed=12466851;

RA The FANTOM Consortium;  
 RT the RIKEN Genome Exploration Research Group Phase I & II Team;  
 RT "Analysis of the mouse transcriptome based on functional annotation of  
 RT 60,770 full-length cDNAs.";

RL Nature 420:563-573(2002).

[2]

RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Brain;  
 RX MEDLINE=21085660; PubMed=11217851;

RA RIKEN FANTOM Consortium;  
 RT "Functional annotation of a full-length mouse cDNA collection.";

RL Nature 409:685-690(2001).

[3]

RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Brain;  
 RX MEDLINE=99279253; PubMed=10349636;

RA Carninci P., Hayashizaki Y.;  
 RT "High-efficiency full-length cDNA cloning.";

RL Meth. Enzymol. 303:19-44(1999).

[4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Brain;

RX MEDLINE=20499374; PubMed=11042159;  
 RA Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,  
 RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;  
 RT "Normalization and subtraction of cap-trapper-selected cDNAs to  
 RT prepare full-length cDNA libraries for rapid discovery of new genes.";  
 RL Genome Res. 10:1617-1630(2000).

[5]

RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Brain;  
 RX MEDLINE=20530913; PubMed=11076861;

RA Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasaki N., Carninci P.,  
 RA Kono H., Akiyama J., Nishi K., Kitsuami T., Tashiro H., Itoh M.,  
 RA Suni N., Ishi Y., Nakamura S., Hazama M., Nishine T., Harada A.,  
 RA Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,  
 RA Fujiwaka S., Inoue K., Togawa Y., Izawa M., Ohara E., Watanabe M.,  
 RA Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunaga S., Kawai J.,  
 RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;

RT "RIKEN integrated sequence analysis (RISA) system-384-format  
 RT sequencing pipeline with 384 multicapillary sequencer.";

RL Genome Res. 10:1757-1771(2000).

[6]

RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=Brain;  
 RA Adachi J., Aizawa K., Akimura T., Arakawa T., Bono H., Carninci P.,

RA Fukuda S., Furuno M., Hasegaki T., Hara A., Hashizume W.,  
 RA Hayashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,  
 RA Hori F., Imotani K., Ishi Y., Itou M., Kagawa I., Kasukawa T.,  
 RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,  
 RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,  
 RA Nishi K., Nomura K., Numazaki R., Ohno M., Ohgaki N., Okazaki Y.,  
 RA Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,  
 RA Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,  
 RA Tagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,  
 RA Tomaru A., Toya T., Yasunishi A., Yamamatsu M., Hayashizaki Y.;

RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AK090178; BAC41125.1; -

SQ SEQUENCE 116 AA; 12691 MW; 4A0D0D56B5409D0A CRC64;

Query Match 81.9%; Score 181; DB 2; Length 116;  
 Best Local Similarity 100.0%; Pred. No. 7.8e-16;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

4 LSELDDRADALQAGASOFETSAAKLRKRYWKXK 38  
 60 LSELDDRADALQAGASOFETSAAKLRKRYWKXK 94

RESULT 12  
 Q9WUW2 PRELIMINARY; PRT; 135 AA.

AC Q9WUW2;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)

DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)

DT 01-NOV-2003 (TREMBLrel. 24, Last annotation update)

DE Vesicle associated membrane protein 2B.

GN Name=vamp2;

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10116;  
 [1]

RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RX MEDLINE=99297576; PubMed=10371166;

RA Mandic R., Lowe A.W.;  
 RT "Characterization of an alternatively spliced isoform of rat vesicle  
 RT associated membrane protein-2 (VAMP-2).";

RL FEBS Lett. 451:209-213(1999).

DR EMBL: AJ13104; CAB43509.1; -

DR InterPro: IPR001388; SynaptoCobrevin.

DR Pfam: PF00957; SynaptoCobrevin; 1.

DR PRINTS: PR00219; SYNAPTOCobrevin.

DR ProDom: PD001229; SynaptoCobrevin; 1.



DR PROSITE: PS00417; SYNAPTOBREVIN; 1.  
 DR PROSITE: PS50892; V-SNARE; 1.  
 SQ SEQUENCE 135 AA; 14509 MW; F37D14A87BDAB16 CRC64;  
 Query Match 81.9%; Score 181; DB 2; Length 135;  
 Best Local Similarity 100.0%; Pred. No. 9.2e-16;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDPRADALQAGASQFETSAAKLKRYKWWKXK 38  
 |||  
 DB 60 LSELDPRADALQAGASQFETSAAKLKRYKWWKXK 94

RESULT 13  
 ID Q8CHRA PRELIMINARY; PRT; 142 AA.  
 AC Q8CHRA; 01-MAR-2003 (TRENBLrel. 23, Created)  
 DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TRENBLrel. 25, Last annotation update)  
 DE Vamp2 protein (Fragment).  
 GN Name:Vamp2;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
 RX MEDLINE=22389257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.W., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Ditchenko L., Mariani K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Tsai T.B., Toshitsuki S., Carninci P., Prange C.,  
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
 RA Bosak S.A., McEwen P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,  
 RA Villalón D.K., Wuzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Maira M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 and mouse cDNA sequences.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;  
 RA Strausberg R.;  
 RT Submitted (NOV-2002) to the EMBL/Genbank/DBJ databases.  
 DR EMBL: BC039745; AAH39745.1; -.  
 DR HSSP: Q9WUW2; ISPC.  
 DR MGD: MGI:1313277; Vamp2.  
 DR GO: GO:0030141; C:secretory granule; IDA.  
 DR GO: GO:0030672; C:synaptic vesicle membrane; IDA.  
 DR GO: GO:0042589; C:zymogen granule membrane; IDA.  
 DR GO: GO:0005516; F:calmodulin binding; IDA.  
 DR GO: GO:0005543; F:phospholipid binding; IDA.  
 DR GO: GO:0000149; F:SNARE binding; IDA.  
 DR GO: GO:001155; F:calcium ion-dependent exocytosis; IDA.  
 DR GO: GO:001157; F:regulation of exocytosis; IDA.  
 DR GO: GO:0016083; P:synaptic vesicle fusion; IMP.  
 DR InterPro: IPR001388; SynaptoBrevin.  
 DR Pfam: PF00957; SynaptoBrevin; 1.  
 DR PRINTS: PR00219; SYNAPTOBREVIN.  
 DR PRODOM: PD001229; SynaptoBrevin; 1.  
 DR PROSITE: PS00417; SYNAPTOBREVIN; 1.  
 DR PROSITE: PS00417; SYNAPTOBREVIN; 1.  
 DR PROSITE: PS50892; V-SNARE; 1.

FT NON TER 1 1  
 SQ SEQUENCE 142 AA; 15313 MW; F1B0C9C9B495B76 CRC64;  
 Query Match 81.9%; Score 181; DB 2; Length 142;  
 Best Local Similarity 100.0%; Pred. No. 9.7e-16;  
 Matches 35; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDPRADALQAGASQFETSAAKLKRYKWWKXK 38  
 |||  
 DB 86 LSELDPRADALQAGASQFETSAAKLKRYKWWKXK 120

RESULT 14  
 ID VAM2\_XENLA STANDARD; PRT; 113 AA.  
 AC P47193;  
 DT 01-NOV-1995 (rel. 32, Created)  
 DT 15-DEC-1998 (rel. 37, Last sequence update)  
 DT 05-JUL-2004 (rel. 44, Last annotation update)  
 DE Vesicle-associated membrane protein 2 (VAMP-2) (SynaptoBrevin 2)  
 DE (SYBII).  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;  
 OC Xenopodinae; Xenopus.  
 OX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Wang X.-H., Poo M.-M.;  
 RL Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE OF 32-113 FROM N.A.  
 RC TISSUE=Embryo;  
 RX MEDLINE=9532445; PubMed=7601005;  
 RA Knecht A.K., Good P.U., David I.B., Harland R.M.;  
 RT "Dorsal-ventral patterning and differentiation of noggin-induced  
 neural tissue in the absence of mesoderm.";  
 RT Development 121:1927-1935 (1995).  
 RL -1- FUNCTION: Involved in the targeting and/or fusion of transport  
 vesicles to their target membrane.  
 CC -1- SUBCELLULAR LOCATION: Type IV membrane protein. Neuronal synaptic  
 vesicles.  
 CC -1- SIMILARITY: Belongs to the synaptoBrevin family.  
 CC -1- SIMILARITY: Contains 1 V-SNARE coiled-coil homology domain.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
 between the Swiss Institute of Bioinformatics and the EMBL outstation -  
 the European Bioinformatics Institute. There are no restrictions on its  
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 modified and this statement is not removed. Usage by and for commercial  
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>  
 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL: AF035017; AAB88138.1; -.  
 DR EMBL: U16801; AAB81376.1; -.  
 DR HSSP: P19065; 1F83.  
 DR InterPro: IPR001388; SynaptoBrevin.  
 DR Pfam: PF00957; SynaptoBrevin; 1.  
 DR PRINTS: PR00219; SYNAPTOBREVIN.  
 DR PRODOM: PD001229; SynaptoBrevin; 1.  
 DR PROSITE: PS00417; SYNAPTOBREVIN; 1.  
 DR PROSITE: PS50892; V-SNARE; 1.  
 KW Acetylation; Coiled coil; Multigene family; Synapse; Synaptoosome;  
 KW Transmembrane.  
 FT INT MET 0  
 FT DOMAIN 91  
 FT TRANSMEM 92 110  
 FT DOMAIN 111 113  
 FT MOD RES 1 1  
 FT DOMAIN 28 88  
 FT SEQUENCE 113 AA; 12341 MW; 6EC6C937B29BC6AB CRC64;  
 By similarity.  
 Cytoplasmic (Potential).  
 Anchor for type IV membrane protein  
 (Potential).  
 Vesicular (Potential).  
 N-acetylsuccinyl (By similarity).  
 V-SNARE coiled-coil homology.

Query Match 81.0%; Score 179; DB 1; Length 113;  
 Best Local Similarity 97.1%; Pred. No. 1,4e-15;  
 Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDPRADALQAGASQFETSAKLRKRYWKNLK 38  
 DB 57 LSELDPRADALQAGASQFETSAKLRKRYWKNLK 91

## RESULT 15

AAH60344 PRELIMINARY; PRT; 114 AA.  
 ID AAH60344;  
 AC AAH60344;  
 DT 02-MAR-2004 (T-EMBLrel. 27, Created)  
 DT 02-MAR-2004 (T-EMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (T-EMBLrel. 27, Last annotation update)  
 DE Vamp2-B-prov protein.  
 GN VAMP2-B-PROV.  
 OS Xenopus laevis (African clawed frog).  
 OC Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
 OC Xenopodinae; Xenopus; Xenopus.  
 CX NCBI\_TaxID=8355;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Embryo;  
 RX MEDLINE=22341132; PubMed=12454917;  
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,  
 RA Richardson P.;  
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus  
 RT Initiative";  
 RL Dev. Dyn. 225:384-391(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Embryo;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Gunaratne P.H.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Kravitski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Maira M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Embryo;  
 RA Klein S., Strausberg R.;  
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC060344; AAH60344.1; -  
 SQ SEQUENCE 114 AA; 12472 MW; AEF2EDCDP2D1DBF CRC64;

Query Match 81.0%; Score 179; DB 2; Length 114;  
 Best Local Similarity 97.1%; Pred. No. 1,4e-15;  
 Matches 34; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 LSELDPRADALQAGASQFETSAKLRKRYWKNLK 38  
 DB 58 LSELDPRADALQAGASQFETSAKLRKRYWKNLK 92

Search completed: November 1, 2004, 17:59:10  
 Job time : 117.625 secs